******	(TM)
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- n.a. database search, using Smith-Waterman algorithm n.a. Srch_nn

Thu Apr 29 02:55:57 1999; MasPar time 500.39 Seconds 1416.800 Million cell updates/sec not generated. Tabular output

Run on:

ggctggagaagaacagcaa......atagctgtgaagacacagaa 300 ccgacctctttttgtcgtt......tatcgacacttctgtgtctt >US-08-968-800-1 (1-300) from US08968800.seq 299 1 ggctggagaagaaacagcaa. Title:
Description:
Perfect Score:
N.A. Sequence:
Comp:

Scoring table:

TABLE default Gap 6

602357 seqs, 1181590623 bases x 2 Searched:

Dbase 0; Query 0

Nmatch STD

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

1:em_ba_2:em_fun_3:em_htg_4:em_hum1_5:em_hum2_6:em_in_7:em_on_8:em_or_9:em_ov_10:em_pat_11:em_ph_12:em_p1_13:em_ro_14:em_un_15:em_v1_9enbank110 Database:

16:gb_bal 17:gb_ba2 18:gb_htg 19:gb_in 20:gb_om 21:gb_ov 22:gb_pat 23:gb_ph 24:gb_pl1 25:gb_pl2 26:gb_pr1 27:gb_pr2 28:gb_pr3 29:gb_ro 30:gb_st 31:gb_sts 32:gb_sy 33:gb_v1

Mean 9.536; Variance 4.385; scale 2.175 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			*P					
	Result No.	t . Score		Query Match Length DB	DB	ID	Description	Pred. No.
	י ט	1 53	17.7	7218	22	166494	Sequence 14 from paten	5.68e-22
	U	2 35	11.7		22	128278	Sequence 5 from patent	1.76e-08
		3 30	10.0	74371	27	AC005369	Homo sapiens chromosom	4.69e-05
	v	4 28	9.4	965	22	AR024229	Sequence 22 from paten	9.58e-04
		5 27	0.6	215	22	128278	Sequence 5 from patent	4.18e-03
	_	6 27	0.6	9.0 7332	26	HUMTAN1	Human TAN-1 mRNA (homo	4.18e-03
	Ü	7 27	0.6	183338	18	HS329A5	Human DNA sequence ***	4.18e-03
	o	8 27	0.6	216021	27	HUAC004787	Homo sapiens Chromosom	4.18e-03
	-	9 26		965	22	AR024229	Sequence 22 from paten	1.78e-02
	Ä	0 26		(7	29	MUSBMP1A	Mus musculus bone morp	1.78e-02
•	H	1 26	8.7	8064	29	MMNOTCHA	M.musculus notch-1 mRN	1.78e-02
	-1	2 26		8221	5	RRNOTCH	R.rattus mRNA homologu	1.78e-02
		13 26		74371	27	AC005369	Homo sapiens chromosom	1.78e-02

SULT 1 166494 7218 bp DNA 166494 1664	er, F	1486 g 1929 t 368 others Score 53; DB 22; Length 7218; Pred. No. 5.68e-22; 173; Mismatches 122; Indels 0; Gaps 0;	TYYXYXYXYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY	126 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY	186 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY	1246 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY
1 166494 2592uence 14 166494 92724471 Unknown. 1 (bases 1 0	from patent US: 1. 1. 1. 1. 1. 1. 1. 1. 1. 1		<pre>/xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx</pre>	<pre>(YYYYYYYYYYYYYYY : : : :: itgagcatgtggccact</pre>	<pre>(YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY</pre>	
ITITION SITON SITO	⊣ 0	BASE COUNT 1944 a ORIGIN Query Match Best Local Similarity Matches 1; Conser		1126 YYYYYYYYYYYYYYY : :::: : 240 cgtagcatctggca		XXXXXXXXXXXXX

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US-08-968-800-1.rge

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Homo sapiens chromosome 5, BAC clone 119j3 (LBNL H175), complete
                                                                                                                                                                                                                                                                    1 (bases 1 to 215)
Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.
Plant inhibitors of fungal polygalacturonases and their use to control fungal disease
Patent: US 556980-A 5 29-OCT-1996;
Location/Qualifiers
120 gcaggitticccggigiatcciggaaagcaictgcaittgittggicccacgcactcacc 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 ctgtgtcttcacagctatactgacagtttatcatggca-catgtcctngagttcacacac 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 gtagcatctggcatgagcatgtggccactgaggcaaaagcacttgtagcttccgtgtgta 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 VNNDSGHNKYSSANYNYGGNNVGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNGGTD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 GNRSGADSYGSSKTAMTSRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 74471)
Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Radner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M., Sequencing of human chromosome 5
Uppublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished

3 (bases 1 to 74371)

Kimmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M.,
Davis, C.A., Kadnar, K., Miguel, T., Pitluck, S., Pollard, M.,
Rojeski, H., Subramanian, S. and Martin, C.H.
Direct Submission
Submitted (01-AUG-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157,
                                 60 aaacttacatccaggttcgcatgtagcttcacagactcccttgctgtttcttctccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 22; Length 215;
Pred. No. 1.76e-08;
64; Mismatches 70; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 KNNGDRNNRYGTGTKSNVSNNCGGGNKRDVSSYANNKCCGSSCT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 ttc-acacatctgtgttggcatggccgggggtttcattccacact 137
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                                                                                                                                 DEFINITION Sequence 5 from patent US 5569830.
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8 c 25 q
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Best Local Similarity 17.1%;
Matches 28; Conservative
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RESULT

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complement(join(38063. 38218,38462. 38578,38741. 38995,39071. 39205,39532. 39630,39935. 40048,40300. 40410,40503. .40661,41868. .41972,42103. .42225,42492. .42569,
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Wallace,T.Paul, Harris,W.J., Carr,F.J., Old,L.J., Welt,S. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /standard_name="histidy1-tRNA synthetase"
/note="78%-100% protein identity GenPept:U18937"
complement(38069. :38215)
/note="GRAIL 2 excellent exon, frame 0"
complement(38462. :38578)
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Pred. No. 9.58e-04;
50; Mismatches 44; Indels 0;
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0
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Pred. No. 4.69e-05;
46; Mismatches 36; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      867 GDYWGGTIVIVSSHIVKDMISSSSASVGDRVIICRSSIIHGNGNIYYWYK 916
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                                                                                        /note="GRAIL 2 excellent exon, frame 2" complement(35238. .35331)
/note="GRAIL 2 excellent exon, frame 1" 36392. .36663
                                                                                                                                                                                                                                                                                                                                                                                          frame 0"
                                                                                                                                                                                      /rpt_family="Alu"
36901. 37222
/note="100% identity EST ou55c09.x1"
/db_xref="dbEST:AI025011"
36901. 37164
/standard_name="STSG-9983"
/db_xref="dbSTS:G26554"
complement(37595. 37654)
/note="GRAIL 2 excellent exon, frame 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 16127 SSSYCKSCCWMMSWRMKKGSWKKRMWWRCRWGMGYSASCSAS 16168
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Recombinant human anti-Lewis b antibodies
Recombinant human anti-Lewis b antibodies
Patent: US 5795961-A 22 18-AUG-1998;
Location/Qualifiers
1. 965
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Sequence 22 from patent US 5795961.
AR024229
93977523
/rpt_family="MLT1"
complement(33670. .33785)
/rpt_family="Alu"
complement(34021. .34144)
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170 c 226 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: remainder of annotations omitted.
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Best Local Similarity 19.6%;
Matches 20; Conservative
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Best Local Similarity 14.5%;
Matches 16; Conservative
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Eukaryotee; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata: Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 7332)
Ellisen, L.W., Bird, J., West, D.C., Soreng, A.L., Reynolds, T.C.,
Smith, S.D. and Sklar, J.
TAN-1, the human homolog of the Drosophila notch gene, is broken by
Chromosomal translocations in Tlymphoblastic neoplasms
91347367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="PID:9338675"
/translation="MPPLLAPLLCLALLPALAARGPRCSQPGETCLNGGKCEAANGTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNACLTNPCRNGGTCDLLTLTEYKCRCPPGWSGKSCQQADPCASNPCANGGQCLPFEA
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YVPCSPSPCQNGGTCRPTGDVTHECACLPGFTGQNCEBNIDDCPGNNCKNGGAVVDGV
NTYNCPCPPEWTGQYCTEDVDECQLMPNACQNGGTCHNTHGGYNCVCVNGWTGEDCSE
NIDDCASAACFHGATCHDRVASFYCECPHGRTGLLCHLNDACISNPCNEGSNCDTNPV
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                                                                                                                                Unclassified.

1 (bases 1 to 215)
Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.
Plant inhibitors of fungal polygalacturonases and their use to
control fungal disease
Patent: US 5569833-A 5 29-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                         92 KTVTDSYNASGTSSSNGGTDGNRSG-ADSYGSSKTAMTSRNRTGKTANNAVDSRNMGDAS 150
                  30-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMTANI 7332 bp mRNA PRI 13-JAN-1995
Human TAN-1 mRNA (homologue of Drosophila Notch gene), 5' end, 9338674
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 4.18e-03;
51; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                           141 others
                  PAT
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128278 215 bp DNA
Sequence 5 from patent US 5569830.
128278
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1. 7332
7. 7332
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Jurkat"
/map="9934.3"
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Best Local Similarity 14.0%;
Matches 16; Conservative
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/partial
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SOURCE
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CLIGGTCODGERGLHECTED SOLE NOGITY OLD INDETICLE POFTUGS TOWN VALUE SERVINGENER THE LENNY THE LITTLE PORT TO THE PROJECT PORT TO THE PROPERTY PORT TO THE PROJECT PORT TO THE PROPERTY PORT TO THE PROPERTY PORT TO THE PROJECT PORT TO THE PROPERTY PORT 
                                                                       TCFCLKGTTGPNCEINLDDGASSPCDSGTCLDKIDDSTCACEPGYTGSMCNSNIDEC
AGNPCINGGTCEDGINGFTCRCPEGYHDPTCLSEVNECNSNPCYTGACRDSLAGYKCD
CDPGWSGTNODINNNECESNPCYNGGTCKDWTSGIVCTCREGFSGPNCGTNINECASN
PCLNKGTCIDDVAGYKCNCLLPYTGATCEVULAPCAPSPCRYNGGEROSDEYSBSCY
PTAGAKGQTCEVDINECVLSPCFRGASCOWTHGXYRCHCQAGYSGRNCETDIDDCRP
NPCHNGSCTGGINTARCDCLPGFRGTFCEEDINECASDPCRNGANCTDCVDSYTCTF
PAGFSGILCENNTPDCTESSCFNGGTCVGGINGTCSCDSRP
PTGFTGHLCQYDVDECASTPCKNGAKCLDGPNTYTCVCTEGYTGTHCEVD
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YETAKVLLDHFANRDITDHMDRLPRDIAQERMHHDIVRLLDEYNLVRSPQLHGAPLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPTLSPPLCSPNGYLGSLKPCVOGKKYRKPSSKGLACGSKEAKDLKARRKKSQDGKGC
LLDSSGMLSPVDSLESPHGYLSDVASPPLLPSPFQQSPSVPLNHLPGMPDTHLGTGHL
NVAAKPEMAALGGGGRLAFETGPPRLSHLPVASGTSTVLGSSSGGALNFTVGGSTSLN
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Submitted (12-NOV-1998) Wellcome Trust Genome Campus, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquires:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 30, 1998 this sequence version replaced gi:3183868.
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of segments is not known; 800 n's separate
segments. Unfinished: dJ329A5 Contig_ID: 01039 acc=297832 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQCEWLSRLQSGMVPNQYNPLRGSVAPGPLSTQAPSLQHGMVGPLHSSLAASALSQMM
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Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 329A5;
297832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNMGRIPLHAAVSADAQGVFQILIRNRAIDLDARMHDGTIPLILAARLAVEGMLEDLI
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Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 183338)
Phillips, S.
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Pred. No. 4.18e-03;
0; Mismatches 15; Indels
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1374 a 2545 c 2268 g 1
Chromosome q34.3.
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Best Local Similarity 73.7%;
Matches 42; Conservative
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HTG; HTGS_PHASE1.
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TITLE
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183 acacggaagctacaagtgcttttgcctcagtggccacatgctc-atgccagatgctacgt 241
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Wallace,T.Paul, Harris,W.J., Carr,F.J., Old,L.J., Welt,S. and
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                                                                                                                                                                           27765. .27672
/note="7766, STS1-cSRL-27g3-uA/cSRL-27g3-uZ, Chr.
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                                                                                                                                                                                                                                                                                                                                                                  chr.
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175801. 175945
//note="16084, CHC.GCT10B02, Chr. -, Homo sapier/db_xref="dbSTS:G09703"
175810. 175845
//note="16316, CHLC.GCT15C04, Chr. -, Homo sapier/db_xref="dbSTS:G09935"
199463. 199572. 199572
//note="9824, WI-3555, Chr. 16, Homo sapiens"
//db_xref="9824, WI-3555, Chr. 16, Homo sapiens"
//db_xref="dbSTS:G04338"
//db_xref="dbSTS:G04338"
//db_xref="dbSTS:G04338"
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Pred. No. 4.18e-03;
60; Mismatches 37; Indels 1;
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                                                                                                                                                                                                                                                                                  /db_xref="dbsTs:G02280"
73826. 73943
/note="7608, sTs1-csRL-24g1-uA/csRL-24g1-u2,
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Recombinant human anti-Lewis b antibodies
Patent: US 5795961-A 22 18-AUG-1998;
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Pred. No. 1.78e-02;
54; Mismatches 44;
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from patent US 5795961
       /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/map="#16q21-22"
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170 c 226 g
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27765. .27872
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Best Local Similarity 9.3%;
Matches 10; Conservative
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Local Similarity 15.4%;
Nes 18; Conservative
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Submitted (24-JUL-1999) The Institute for Genomic Research, 9712

Medical Center Dr., Rockville, MD 20850, USA

Medical Center Dr., Rockville, MD 20850, USA

On Jul 24, 1998 this sequence version replaced gi:3241936.

Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA e-mail address: humgenetigr.org. The orientation of the sequence is from SP6 end to T7 end Genes were identified by a combination of five methods including: XGRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.Edu/-chris/GENSCANW.html)searches of the complete sequence against a peptide database, and the Human gene Index database at TIGR (http://www.tigr.org/tdb/hgi/hgi.html).

Genes without pepetide homolgy having spliced EST hits are termed 'Unknown gene product', Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).

Location/Qualifiers

Ince
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HOMO sapiens Chromosome 16 BAC clone CIT987SK-A-952F10, complete
sequence.
2002 bp Unfinished: dJ329A5 Contig_ID: 03639 acc=297832 Length: 55652 bp Unfinished: dJ329A5 Contig_ID: 04239 acc=297832 Length: 21109 bp Unfinished: dJ329A5 Contig_ID: 03867 acc=297832 Length: 2332 bp Unfinished: dJ329A5 Contig_ID: 00527 acc=297832 Length: 96075 bp Unfinished: dJ329A5 Contig_ID: 04002 acc=297832 Length:
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1 (bases 1 to 216021)
Adams, M.D., Loftus, B.J., Zhou, L., Crosby, M., Fuhrmann, J., Mason, T.M., Brandon, R., Kim, U.J., Kerlavage, A.R. and Venter, J.C. Homo, sapiens Chromosome 16 BAC clone CIT987SK-A-952F10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams,M.D. and Loftus,B.J.
Direct Submission
Submitsed (02-JUN-1998) The Institute for Genomic Research, 9712
Medical Center Dr. Rockwille, MD 20850, USA, Email:
                                                                                                                                                                                                                                                                                                                   * This sequence is unfinished. When sequencing is complete,
    * the sequence data presented in this record will be replaced
    *by a single finished sequence with the same accession number.
    Location/Qualifiers
    1. .183338
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /chromosome="6"
/clone="329A5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 catgtggccactgaggcaaaagcacttgtagcttccgtgtgtattcacacatctgtg 166
                                                                                                                                                                                                                                                    *** WARNING: Phase 1 High Throughput Genome Sequence ***
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 18;
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Adams, M.D. and Loftus, B.J.
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Best Local Similarity 73.7%;
Matches 42; Conservative
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Ludses, I to 29/0)

Fukagawa, M., Noboru,S., Hogan,B.L.M. and Jones,C.M.
Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1)
which is related to the Drosophila dorsoventral gene toiloid and
encodes a putative astain metalloproteinase
Dev. Biol. 163, 175-183 (1994)
94229342
On Jan 6, 1994 this sequence version replaced gi:437434.

Location/Qualifiers
1. 2976
/Strain="Mus musculus"
/Strain="S75BL/6"
      Mus musculus bone morphogenetic protein (Bmp-1) mRNA, complete cds
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IQSPNYPDDYRPSKVCIWRIQYSEGFHYGLIPROSFEIERHDSCAYDYLEVRDGHSESS
NLIGRYCGYENPDDIKSTSSRLWLKFVSDGSINKAGFAVNFFKRVDECSRPNKGGCEO
RCLNTLGSYKCSCDPGYELAPDKRRCEAAGGGFLTKLNGSITSPGWPKEYPPNKNCIW
QLVAPTQYRISLQFDFFFTGGNDVCKYDFVEVRSGITADSKIHGKFCGSERPEVITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="PID:9439507"
/translation="MPGVARPPLPLSLPLLLLLLLPARRPAAGLGRLHLRPGRGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGAPOLORPLOGGCLFWDIALDEEDLRAFQVQQAAVLROOTARRPSIKAAGNSSALGG
QGTSGQPQRESRGRWRGRPRSRRAATSRPERVWPDGVIPFVIGGNFTGSQRAVFRQAM
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YARWIFSRGIFLDTIVPKYEVNGVKPSIGORTRLSKGDIAQARKLYKCPACGETLODS
TGNFSSPEYPNGYSAHMHCVWRISVTPGEKIILNFTSMDLYRSRLCWYDYVEVRDGFW
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HDNKHDCKEAGCEHKVTSTSGTITSPNWPDKYPSKKECTWAISSTPGHRVKLFFVEMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FQASHSTECGGQVRADVKTKDLYSHAQFGDNNYPGGVDCEWVIVAEEGYGVELVFQTF
EVEEETDCGYDYIELFDGYDSTAPRLGRYCGSGPPEEVYSAGDSVLVKFHSDDTISKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I ESQPECAYDHLEVFDGRDAKAPVLGRFCGSKKPEPVLATGNRMFLRFYSDNSVQRKG
                                                                                                        Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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bone morphogenetic protein-1; metalloproteinase.
Mus musculus (strain C57BL/6) embryo cDNA to mRNA.
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Pred. No. 1.78e-02;
0; Mismatches 16; Indels
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Best Local Similarity 72.4%;
Matches 42; Conservative
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1 (bases 1 to 8064)
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NATURAL ASARAH, ENGHAL FILDER PROFIT SULLE FILLER F
del Amo, F.F., Gendron-Maguire, M., Swiatek, P.J., Jenkins, N.A., Copeland, N.G. and Gridley, T. Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of Drosophila Notch Genomics 15 (2), 259-264 (1993)
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NTYNCRCPPEVTGQYCTEDVDECQLMPNACQNAGTCHWHGGYNCVCVNGWTGEDCSE
NIDDCASAACFQGATCHDRVASFYCECPHGRTGLLCHIKHACISNPCNEGSNCDTNPV
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Direct Submission
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EIDNRQCVQSSSQCFQSATDVAAFLGALASLGSLNIPYKIEAYKSEVVEPPLPSQLHL
MYVAAAAFVLLFFVGGGYLLSKRRRQHGQLWFPEGFKVSEASKKRREPLGEDSVGL
KPLKNASDGALMDDNONEWGDBDLEFYKKFRFEEPVVLPDLSDQTDHRQWTQQHLDAAD
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RCEGDVNECLSNPCDPRGTQNCVQRVNDFHCECRAGHTGRRCESVINGCRGKPCKNG
VCAVASNTARGFICRCPAGFEGATCENDARTGGSLRCLNGGTCISGPRSPTCLCLGSF
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GPDIPPPQIEEACELPECQVDAGNKVCNLQCNNHACGWDGGDCSLNFNDPWKNCTQSL
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BCEWDGLDCAEHVPERLAAGTLVLVVLLPPDQLRNNSFHFLRELSHVLHTNVVFKRDA
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DSLESPHGYLSDVASHPLLPSPFQQSPSMPLSHLPGMPDTHLGISHLNVAAKPEMAAL
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Location/Qualifiers
1. .8064
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/dev_stage="embryonic day
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/product="notch-1"
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/db_xref="PID:e1291872"
/db_xref="PID:e1291872"
/db_xref="PID:g3123945"
/translation="MPRLIAPLICHTLIPALAARGLRCSQPSGTCLNGGRCEVANGTE
ACVCSGAFVGQRCQDPSPCLSTPCRNAGTCYVVDHGGIVDYACSCPLGFSGPLCLTPL
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YLCLCLKGTTGPNCEINLDDCASNPCDSGTCLDKIDGYECACEPGYTGSMCNVNIDEC
GWVPSQYNPLRPGVTPGTLSTQAAGLQHSMMGPLHSSLSTNTLSPIIYGLPNTRLÄT
OPHLVQTQOVQPQNLPLQDQNLQPDSPSQPHLSVSSAANGHIGKSFLSGBPSQANVQPLG
PSSLPVHTILPQESQALPTSLPSSMYPPMTTQPLTPPSGHSYSSSPVDNTPSHQLQV
PEPTPLTPSPESPPOMSSSSPHSNISONSEGISSPPTTPRSQIIHIPERFR
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Location/Qualifiers
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1 (bases 1 to 8221)
Weinmaster,G., Roberts,V.J. and Lemke,G.
A homolog of Drosophila Notch expressed during mammalian
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                                                                                                                                                                                                                                                                                     Length 8064;
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R.rattus mRNA homologue of Drosophila notch protein.
X57405
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Pred. No. 1.78e-02;
0; Mismatches 16; Indels
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241. .7836
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/db_xref="taxon:10117"
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Weinmaster, G.
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Weinmaster, G.
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Best Local Similarity 72.4%;
Matches 42; Conservative
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black rat.
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YKCSCPRGTQGVHCEINVDDCHPPLDPASRSPKCFNNGTCVDQVGGYTCTCPPGFVGE
RCEGDVNECLSNPCDPRGTQNCVQRVNDFHCECRAGHTGRRCESVINGCRGKPCRNGG
                                                                          VCAVASNTARGFICRCPARFEGATCENDARTCGSLRCLNGGTCISGPRSPTCLCLGSF
TGPECQFPASSPCVGSNPCYNQGTCEPTSESPFYRCLCPAKFNGLLCHILDYSFTGAA
                                                                                                                                                        GRDIPPPQIEEACELPECQEDAGNKVCNLQCNNHACGWDGGDCSLNFNDPWKNCTQSL
QCWKYFSDGHCDSQCNSAGCLFDGFDCQLTEGQCNPLYDQYCKDHFSDGHCDQGCNSA
ECEWDGLDCAEHVPERLAAGTLVLVVLLPPDQLRNNSFHFLRDVSHVLHTNVVFKRDA
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QPHLVQTQQVQPQNLQIQPQNLQPPSQPHLSVSSAANGHLGRSFLSGEPSQADVQPLG
PSSLPVHTILPQESQALPTSLPSSMVPPMTTTQFLTPPSQHSYSSSPVDNTPSHQLQV
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1 (bases 1 to 74371)

Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Radner,K., Miller,C., Pitluck,S., Pollard,M., Rojeski,H., Subrammanian,S. and Martin,C.H.
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Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Davis,C.A., Kadner,K., Miguel,T., Pitluck,S., Pollard,M., Rojeski,H., Subramanian,S. and Martin,C.H.
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'db_xref="taxon:9606"

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8258. .8503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tandard_name="possible repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (9740. 9845)
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complement (10440. .11015)
/rpt_family="Alu"
11950. .12250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (16675. .16977)
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3707. 3728
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4366. 4661
                                                                                                                                                                                                                                      4366. .4661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="Alu"
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12365. .12645
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/rpt_unit=AC
/rpt_unit=AC
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727. .13750
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rpt_unit=T
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join(29485. .29559,29598. .29779)

/note="95% identity dbsTs:G14522 (SHGC-11312)"

/standard_name="Al027942"

/note="100% identity EST ov84al0.x1"

complement(30401. .30536)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89712. .28930

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:complement(88769. .28838)

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:8987. .29214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(34021. .34144)
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complement(35238. .35331)
                                                                                                                                                                                                                                                                                                         standard_name="possible repeat"
8022. .23326
                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(24639. .24694)
/rpt_family="MER42"
complement(25349. .25713)
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                              .22981)
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                                                                                                                                21202. 21496
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21736. 22035
/rpt_family="Alu"
22017. 22010
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23744. .23767
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32977, 33088
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1202 21496
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774. .28057
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8712. .289
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                                                                                                      36901. :310053::n102011
36901. :310053::n102011
36901. :31005554
/db_xref="dbage="STSG-9983"
/db_xref="dbage="STSG-9983"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepatitis C-like viruses.
1 (bases 1 to 565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSUCHECALD KAZUBKI, C., HITOMICTSU, K. and Yataro, I.
NUCLEIC ACID FRAGMENT WITHIN ENVELOPE REGION OF HEPAITIES C VIRUS
NUCLEIC ACID FOR DETECTING THE SAME
PALENT: JP 1992349885-A 1 04-DEC-1992;
TEIJIN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 tgtggccactgaggcaaaagcacttgtagcttccgtgtgtattcacacatctgtgttggc 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E04076 565 bp RNA PAT 26-NOV-1996

GDNA encoding envelope region of type C hepatitis virus.

E04076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
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PF 29-MAY-1991 UP 1991152169
PI MORINAGA TSUTAE, CHAYAMA KAZUAKI, KUMADA HIROMITSU, ICHIKAWA YATARO
PC C12015/10,C1201/68,C1201/70//C1201/201/CC strandedness: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 atggccggggtttcattccacactcattcacatcttgactgcaggttttcccg 108
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 26; DB 27; Length 74371;
Pred. No. 1.78e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      64; Mismatches 40; Indels
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/note="GRAIL 2 excellent exon, frame 1" 36392. .36663
                               35901. .37222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25; DB 22;
Pred. No. 7.37e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Hepatitis C virus"
/db_xref="taxon:11103"
93 c 107 g 85 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40; Mismatches
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Best Local Similarity 28.2%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.7%;
Best Local Similarity 7.1%;
Matches 8; Conservative
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JP 1992349885-A/1.
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Hepatitis C virus
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                         repeat_region
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212 YVATCMTGCWYDYYCCBGGGTGYRYBCCYTGYGTYCGSGARRYRRYNNYTCBMGNTGYT 271

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YAMAMOTO SHUJI, SUZUKI KOJI
PC CO7H21/04, A61K38/00, C12N15/09, C12P21/02, (C12P21/02, C12R1:91);
CC strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PR
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/cell_type='epithelial cell'
1. .816
/product='Soluble thrombin binding protein'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAVING ACTION PROMOTING
                                                                                                                                                                                           E12212 816 bp DNA PAT 27-APR-1998 Human cDNA encoding a soluble thrombin binding protein by which stimulates protein C activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OS Homo sapiens (human)
PN JP 1996291193-A/5
PD 05-NOY-1996
PF 08-JAN-1988 JP 1996138587
PR 08-JAN-1987 JP 87P 1065,
PR 08-JAN-1987 JP 87P 1066,
PR 08-JAN-1987 JP 87P 144081,
11-JUN-1987 JP 87P 305876,
PR 04-DEC-1987 JP 87P 305876,
PR 04-DEC-1987 JP 87P 305878 PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GACGTGGATGACTGCATACTGGAGCCCAGTCCGTGTCCGCAGCGCTGTGTCAACACACAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::|| : :::: |:| |: ::||: |:| |: |:|| 137 tcattcacatcttgactgcaggttttcccggtgtatcctggaa-agcatctgcatttgt 79
                                                                                                                                                                                                                                                                                                                                                                Districts, Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases I to 816)

Yamamocto, S. and Suzuki, K. .

MEDICINAL COMPOSITION CONTAINING PEPTIDE HAVING ACTION PROMOTY ACTIVATION OF PROTEIN C BY THROWBIN
PATENT: JP 1996291193-A 5 05-NOV-1996;
ASAHI CHEM IND CO LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                            Length 816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 25; DB 22; Length 816
Pred. No. 7.37e-02;
0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism='Homo sapiens'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
297 c 248 g 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    completed: Thu Apr 29 03:04:25 1999
ne : 508 secs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 topology: Linear;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.4%;
ilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                               g3251046
JP 1996291193-A/5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 6
                                                                                                                                                                                                                                                                                                                            Homo sapiens.
Homo sapiens
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

 n.a. database search, using Smith-Waterman algorithm п.а. srch_nn Sat Apr 24 22:26:11 1999; MasPar time 60.26 Seconds 677.328 Million cell updates/sec not generated. Tabular output

qu on:

>US-08-968-800-1 (1-300) from US08968800.seq 299 Description: Perfect Score: N.A. Sequence: Title:

1 ggctggagaagaaacagcaa.......atagctgtgaagacacagaa 300 ccgacctcttctttgtcgtt.......tatcgacacttctgtgtgtctt Comp:

TABLE default Scoring table:

Dbase 0; Query 0 Gap STD Nmatch 188442 seqs, 68026449 bases x 2 Minimum Match 0% Listing first 45 summaries Post-processing: Searched:

Database:

n-geneseq32
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part40

Mean 7.783; Variance 4.414; scale 1.763 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		p					
Result No.	t . Score	~ –	Query Match Length DB	DB	ID	Description	Pred. No.
1	1 40	13.4			N81164	Base substituted E.co	1.16e-11
O	2 40	13.4	204	~	N81164	Base substituted E.co	1.16e-11
	3 37	12.4		σ	051746	Oligonucleotide probe	8.71e-10
υ	4 37	12.4	91	σ	051746	Oligonucleotide probe	8.71e-10
υ	5 32	10.7	114	12	070469	Generic DNA sequence	9.60e-07
υ	6 32	10.7		12	070468	Generic DNA sequence	9.60e-07
U	7 30	10.0		12	070465	Generic DNA sequence	1.46e-05
υ	30	10.0	114	12	070467	Generic DNA sequence	1.46e-05
O	9 29			13	070470	Generic DNA sequence	5.60e-05
0	0 29			12	070466	Generic DNA sequence	5.60e-05
1	1 27			12	070465	Generic DNA sequence	7.85e-04
Н	2 27	0.6		12	070468	Generic DNA sequence	7.85e-04
H	3 25	8.4		12	070469	Generic DNA sequence	1.03e-02

00000	1.03e-02 1.03e-02	36	1.03e-02	ge'	1.03e-02		1.03e - 02	1.03e-02	1.03e-02	1.03e - 02	1.03e-02	1.03e-02	1.03e-02	1.03e - 02	1.03e-02	1.03e-02	1.03e - 02	1.03e-02	1.03e-02	1.03e-02	3.63e-02	9.	3.63e-02	3.63e-02	5e-	1.25e-01
Ġ Ġ ⊢	encoding	Sequence encoding thr	cDNA encoding human r	equence encoding	Encodes truncated hum	Encodes thrombomoduli	Ũ	Encodes thrombomoduli	Soluble thrombomoduli	Thrombin-binding subs	Encodes thrombomoduli	Recombinant thrombin-	Human thrombomodulin	Human thrombomodulin	Sequence encoding thr		coding	g	2.1	Hind III - Not I thro	Generic DNA sequence	Generic DNA sequence	Generic DNA sequence	ric DN	DC43 TSAR library gen	Human IL-8 receptor-a
Q70467 Q70472 T76405 Q05947	Q05948 Q05946	005945	T14656	005973	020811	095956	T14654	095958	010435	013406	095957		T12792			_				_			070473	97047	T1361	T76368
12 12 32 1		٦;	21		m	16	21	16	N	~	16	4	21	ø	Н	m	N	Н	-	ω	12	12	12	12	21	32
114 114 178 720	726	759	825	831	1425	1482	1491	1529	1545	1656	1680	1680	1946	2011	2313	2463	3373	3573	3640	6977	114	114	114	114	81	140
88888 4444	8 8 4 4	•	ω α 4. <		8.4		8.4	8.4	8.4	8.	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4						8.0		7.7
52 52 52 52	25 25	25	25 5.5	25	52	22	22	52	22	22	25	22	22	22	22	22	25	52	52	52	24	54	77	54	23	23
14 15 17	18 19	20	21	23	24	25		27	28	59	30	31	32	33	34	32	36	37		36	40	41	42	43	44	45
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ALIGNMENTS

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Now War 1988; 105163.

No. 27-ARI-1988; 105163.

No. 30-APR-1988; 105163.

No. 30-APR-1987; US-034819.

No. 30-APR-1987; US-03-APR-1987; US-0
                                                        N81164;
08-NOV-1990 (first entry)
asse substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
                                                                                                                                                                                                                                                                                        /function-multiple cloning site
187.204
/*tag= b
                                                                                                                                                                                                              Location/Qualifiers
                            standard; DNA; 204 BP.
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                                                                                                                                                                                                                                             19..69
/*tag=
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Sequence 204 BP;
                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                            EP-285123-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-1988,
                                                                                                                                                                                                                                                                                                                                    primer_bind
   T 1
N81164
RESULT
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108 Others;

11 T;

17 G;

47 C;

21 A;

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WPI: 88-27992740.

Thirducing random point mutations into nucleic acods -

Thy prepn of single stranded template, annealing a primer, elongation, or prepn of single stranded template, annealing a primer, elongation, or standom point mutations were introduced into the alpha fragment of Bisclosure; p; English.

S Disclosure; p; English.

C Random point mutations were introduced into the alpha fragment of Single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all consible nucleotide positions within a specified region. The rerse transcriptase and the molecules are misincorporated by the transcriptase and the molecules are completed to forms that can be multiplied and then expressed in a suitable dormal the molecules are completed to forms that can be concurred singularly in any given mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                               78 dchvgccgymrttthhyrrmrbnvyrdynrsdaawyccyrrsvkydccynachhddhyv 137
                                                                                       87 mrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvh 146
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 cactcattcacatcttgactgcaggttttcccggtgtatcctggaaagcatctgcatttg 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                  N81164;
08-NoV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 T; 108 Others;
                                           ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P. Knowles J. Koivula A. Bamford J. Reinikainen T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
        Length 204;
                                      34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.4%; Score 40; DB 1; Length 204; Larity 9.2%; Pred. No. 1.16e-11; Conservative 53; Mismatches 36; Indels
                                                                                                                                 138 ybbbvynvhnhnncncccbnnhvchnvhbnnhrnwayvrhd 178
                                                                                                                                                                 174 tgtgaatacacacggaagctacaagtgcttttgcctcagtg 214
 Score 40; DB 1; L
Pred. No. 1.16e-11;
54; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                             19..69
/*tag= a
/*function=multiple cloning site
187..204
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 nhnncncccbnnhvchnvhbnnhrnwayvrhdarrddv 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 G;
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 C;
                                                                                                                                                                                                                      T 2
N81164 standard; DNA; 204 BP.
 Match 13.4%;
Local Similarity 11.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .T 3
Q51746 standard; cDNA; 91 BP.
                                    12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 BP; 21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAY-1988.
30-MAR-1988; 105163.
03-APR-1987; US-0348
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                                                                                                                                                                                                                                                                                                                                                         misc_feature
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                051746;
                                 Matches
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Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                               for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
                                                                                                                             Samples Claim 3; Page 14; 23pp; English.

Claim 3; Page 14; 23pp; English.

Oligonucleotide probe MX14-A consists of nucleotides 5-95 of N (051735). It hybridized to all spp. of mycobacteria tested, I cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also 051735-45 and 051747-59.

See also 051735-45 and 051747-59.
                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligoniclectide probe MK14-A consists of nucleotides 5-95 of (051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                    New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                       9
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Pred. No. 8.71e-10;
43; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                            10 gssvhsyyvvhvvshhhsvhhvvhvhvvvvhhvvhvvhhvyvsv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.4%; Score 37; DB 9; Length 91; 2.0%; Pred. No. 8.71e-10; vative 43; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 gssvhsyyvvhvvshhhsvhhvvhvsvvvvhhvvhvvhvhyhvyvsv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       standard; cDNA; 91 BP.
                                                         (BECT ) BECTON DICKINSON CO. Shank DD, Spears PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
Shank DD, Spears PA;
WPI; 93-378844/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q70469 standard; DNA; 114 BP. Q70469;
                                                                                                                                                                                                                                                                      12.4%;
                                                                                                                                                                                                                                                                                                   1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Conservative
                           24-MAY-1993; 108325.
26-MAY-1992; US-889651
                                                                                    WPI; 93-378844/48.
New oligo:nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAY-1993; 108325
                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP-571911-A.
01-DEC-1993.
EP-571911-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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Q51746 :
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55..60

misc_feature

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Screening a recombinant vector intrary expressing fusion proteins

Screening a recombinant vector intrary expressing fusion proteins

PS Comprising a binding domain and an effector domain

Disclosure; Page 35, 255pp; English.

CG 70468 is a generic DNA Sequence used to generate random TSAR (Totally

Synthetic Affinity Reagents) peptides. This generic formula can also be

CG represented as follows: X(NNB)11(TGC)(NNB)7(TGC)(NNB)10Y. X

CG and Y are flanking restriction sites (X is not the same as Y) that are

CG represented as follows: X(NNB)11(TGC)(NNB)7(TGC)(NNB)10Y. X

CG of the specific peptides generated by these generic sequences are shown in

CG RESISI-54. TSABS are concatenated heterofunctional proteins or peptides,

CC omprising at least two functional regions - a binding domain with

CC Affinity for a ligand and a second effector peptide portion that is

CC chemically or biologically active. They may further comprise a linker

CC Affinity for a ligand and a second effector peptide portion that is

CC Affinity for a ligand contains 2 or 4 cysteine residues positioned

CC That the expressed peptide contains 2 or 4 cysteine residues positioned

CC Thanking, the unpredicted or variant residues. These residues

CC onfer some degree of conformational rigidity to the peptides.

CC deliver a chemically or biologically active moiety, eg. metal ion,

CC adioisotope, peptide, toxin or enzyme, to the specific target or on the

CC monoclonal or polyclonal antibodies and therefore circumvent the need

CC conformation. The TSARs are easily characterised and have designed activity

CC allowing direct and rapid detection in a screening process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 cacttgtagcttccgtgtgtattcacacatctgtgttggcatggccggggtttcattcca 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affility reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 banbanbanbanbanbanbanbanbanbanbtgcanbanbanbanbanbanbananana 62
                                                                                                                                                                                       Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 banbanbanbanbanbanbtgcanbanbanbanbanbanbanbanbanb 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32; DB 12; Length 114; Pred. No. 9.60e-07;
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5, 9 or 12 nucleotides (see
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; US-176500.
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V NORTH CAROLINA.
Kay BK;
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(UVNC-) UNIV NORTH CAROLINA.
FOWIKES DM, RAY BK;
WPI: 94-279739/34.
P-PSDB; R65154.
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P-PSDB; R65150 and R65151.
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US-176500.
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31-JAN-1994;
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     While yet 2/19/34.4.

Identifying proteins or peptide(s) which bind a ligand - by
Identifying proteins or peptide(s) which bind a ligand - by
Screening a recombinant vector library expressing fusion proteins
Disclosure; Page 35; 255pp. English.

Disclosure; Page 35; 255pp. English.

O70669 is a generic DNA sequence used to generate random TSAR peptide
This generic Cormula can be represented as follows; XTGC)(NNB)10-

(TGC)(NNB)6Z(NNB)2(TGC)(NNB)14(TGC)Y. A and Y are flanking restriction
sites (X is not the same as Y) that are not specified further. Thiss
concare generic sequences are shown in Q70465-68. Other specific peptides

CG generic sequences are shown in Q70465-68. Other specific peptides

CG generated by these generic sequences are shown in R65150-54. TSARs are

CO concatenated heterofunctional proteins or peptides, comprising at least

CG generated by these generic sequences are shown in R6510-14. TSARs are

CO concatenated heterofunctional proteins or peptides, comprising at least

CG generated by these generic sequences are shown in R6510-14. TSARs are

CO concatenated heterofunctional proteins or peptides, comprising at least

CG concatenated heterofunctional proteins or peptides between the 2 domains.

CA second effector peptide portion that is chemically or biologically

CC active. They may further comprise a linker peptide between the 2 domains.

CC ontains 2 or 4 cysteine residues positioned in, or flanking, the

CC conformational rigidity to the peptides. The TSARs or compose, comprising

CC conformational rigidity to the peptides. The TSARs or compose, comprised

CC a TSAR binding domain can be used in vivo to deliver a chemically or

CD biologically active molety, eq. metal ion, radioisotope, peptide, toxin

CC conformation or in vivo antibody production. The TSARs are easily

CC characterised and have designed dor complexes and trabedian process

CC characterised and have designed activity allowing direct and rapid
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sequence of 6,9 or 12 nucleotides (see
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Sequence 114 BP; 0 A; 4 C
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Q70468 standard; DNA; 114 BP.
Q70468;
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31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Ray BK;
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8.0%;
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US-176500.
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01-FEB-1994; U00977.
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Matches

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Indels

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Tdentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins by comprising a binding domain and an effector domain by bisclosure; Page 35, 255pp; English.

CC 70465 is a generic DNA sequence used to generate random TSAR (Totally compresented as follows: X(NNB) 12(NNB) 14(TGC)(NNB) 3Y. X and X are flanking restriction sites (X is not the same as Y) that are concatenated proteins or peptides. The sequences are shown in 070466-68.

CC not specified further. Other generated by these generic sequences are shown in 070466-68.

CC omprising at least two functional regions - a binding domain with comprising at least two functional proteins or peptides, affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker chemically or biologically active. They may further comprise a linker comprise a ligand and a second effector peptide portion that is chemically or biologically active molectical are also designed conformational righlity to the peptides. They see a linker confer some degree of conformational righlity to the peptides. They can else of conformational righlity to the peptides. They can also replace the function of macromolecules, eg. conformational antibodically active molety, eg. metal ion, radiolsotope, peptide, toxin or enzyme, to the specific target or on the monclonal or polyclonal antibodies and therefore circumvent the need conformation and antibodies and therefore circumvent the need conformation and polyclonal antibodies and therefore circumvent the need conformation and right of mean and the activity allowing direct and rapid detection in a screening process.
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TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; synthetic.
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sequence of 6, 9 or 12 nucleotides (see
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31; Mismatches 77; Indels
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Pred. No. 1.46e-05;
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Conservative
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05-APR-1995
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070467 is a generic DNA Sequence used to generate random ISAR (Totally Synthetic Affinity Reagents) peptides.This generic formula can also be represented as follows: X(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)1Y. X

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and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68.

C their specified peptides generated by these generic sequences are shown in C R65131-54. TSARS are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is cemically or biologically active. They may further comprise a linker of peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compans. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, cadioisotope, peptide, toxin or enzyme, to the specific target or on the conformal and also replace the function of macromolecules, eg. metal ion, monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production.

The TSARs are easily characterised and have designed activity allowing
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2070470 is a generic DNA Sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)4(CAC)(NNB)8C(NNB)6(CAC)(NNB)8 (CAC)(NNB)8 (CAC) (NNB)8 (CAC) (NNB)8 (CAC) (NNB)8 (CAC) (NNB)8 (NNB)8
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/note= "encoded by Z (see comments)"
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31; Mismatches 77
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30-DEC-1993; US-176500,
31-JAN-1994; US-189331,
(UNC-) UNIV NORTH CAROLINA.
FOWIKES DM, KAY BK;
WPI: 94-279739/34.
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Conservative
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Best Local Similarity
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Terbusis (NOS) 2.0.

Terening a recombinant vector library expressing fusion proteins screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain proteins building domain and an effector domain bisclosure; Page 35; 255pp; English, control and an effector domain bisclosure; Page 35; 255pp; English, control and an effector domain control as generic DNA sequence used to generate random TSAR (Totally Control as a generic DNA sequence used to generate as an also be represented as follows:X(NNB)1(TCC)(NNB)10(TGC)2(NNB)42(NNB)8(TGC)(NNB) CCC 197. X and Y are flanking restriction sites (X is not the same as Y) that are not specific peptides generated by these generic sequences are shown in R65151-34. TSARS are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding continuity affinity for a ligand and second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also continued in, or flanking, the unpredicted or variant residues. These positioned in, or flanking, the unpredicted or variant residues contents compens. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production.
deliver a chemically or biologically active molety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP, 5 A, 10 C, 0 G, 0 T;
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Pred. No. 5.60e-05;
28; Mismatches 69; Indels
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/note= "this sequence represents 'Z'; Z
sequence of 6, 9 or 12 nucleotides (see
comments)"
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5.8%;
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US-189331.
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WPI; 94-279739/34.
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31-JAN-1994;
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Tentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins of comprising a binding domain and an effector domain by screening a recombinant vector library expressing fusion proteins or pusiciosure; Page 35, 25pp; English.

Olde5 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)6(TGC)(NNB)11Z(NNB)14(TGC)(NNB)3Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68.

Other specified further. Other generic sequences are shown in R65151-44. TSARs are concatenated by these generic sequences are shown in R65151-44. TSARs are concatenated by these generic sequences are shown in R65151-44. TSARs are concatenated by these generic sequences are shown in CR6151-44. TSARs are concatenated by these generic sequences are shown in CR6151-44. TSARs are concatenated by these generic sequences are shown in CR6151-44. TSARs are aligand and as accord effector peptide portion that is chantically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so confer some degree of conformational rigidity to the peptides. The TSARs or compens. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal ion, and aniologically active molety, eg. metal ion, and complex methods of hybridoma antibodies and therefore circumvent the need for complex methods of hybridoma and therefore circumvent the need for complex methods of hybridoma and herefore circumvent the need for complex are easily characterised and have designed and have designed and have designed and part of the production. The TSARs are easily characterised and have designed and part 
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                                                                                                                                                                                                                                                                                                                                                                                                                      domain;
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                                                                                Gaps
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/note= "this sequence represents
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Pred. No. 7.85e-04;
29; Mismatches 79;
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Q70465 standard; DNA; 114 BP
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
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Best Local Similarity 3.6%;
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6.4%;
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                                         Query Match
Best Local Similarity
  114 BP;
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PT Screening a Lecombinant vector library expressing fusion proteins
PT Comprising a binding domain and an effector domain
Disclosure; Page 35; 255pp; English.

CC Synthetic Affinity Reagents) peptides. This generate random TSAR (Totally
CC Synthetic Affinity Reagents) peptides. This generate for an also be
CC crepresented as follows: X(NNB)11(TGC)(NNB)6Z(NNB)(TGC)(NNB)10v. X

CC and Y are flanking restriction sites (X is not the same as Y) that are
CC other specific peptides generated by these generic sequences are shown in
CC other specific peptides generated by these generic sequences are shown in
CC other specific peptides generated by these generic sequences are shown in
CC affinity for a ligand and a second effector peptide portion that is
CC efficient the Z domains. The oligonucleotides are also designed so
in, or flanking, the unpredicted or variant residues. These residues
CC comprising a TSAR binding domain can be used in vivo to
CC comprising a TSAR binding domain can be used in vivo to
CC compsons. comprising a TSAR binding domain can be used in vivo to
CC addiver a chemically or biologically active moiety, eg. metal ion,
CC cell. They can also replace the function of macromolecules, eg.
CC complex methods of hubridoms function of macromolecules, eg.
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Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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/note= "this sequence represents 'Z'; Z can
sequence of 6, 9 or 12 nucleotides (see
comments)"
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UVINC.) UNIV NORTH CAROLINA.
FOWINCS DM, KAY BK;
WPI; 94-279739/34.
P-PSDB; R65154.
Identifying proteins or peptide(s) which bind a ligand screening a recombinant vector library expressing fusion screening a recombinant vector library.
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Pred. No. 7.85e-04;
29; Mismatches 79;
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Q70468 standard; DNA; 114 BP.
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63 bnnbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnb 114 | i i i i i i i i i i 234 tgctacgtgtgtagaactcnaggacatgtgccatgataaactgtcagtatagc 285

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PT screening a recombinant vector library expressing fusion proteins
PT comprising a binding domain and an effector domain
Disclosure; Page 35; 255pp; English.

COMPAGE 1s a generic DNA sequence used to generate random TSAR peptide
CTGC(NNB) ZG(NNB) ZG(NNB) 14(TGC)Y. X and Y are flanking restriction
Sequence generates peptides that are clovarieaf in structure. This
sequence generates peptides that are clovarieaf in structure. Other
CG stes (X is not the same as Y) that are not specific peptides
CG generated by these general sequences are shown in R05150-54. TSARs are
CG enerated by these general sequences are shown in R65150-54. TSARs are
CG conclenated heterofunctional proteins or peptides, comprising at least
CG a second effector peptide portion that is chemically or biologically
CG two functional regions - a binding domain with affinity for a ligand and
active. They may further comprise a linker peptide between the 2 domains.
CG contains 2 or 4 cysteine residues positioned in, or flanking, the
CG conformational rigidity to the peptides. The TSARs or comprising
CG a TSAR binding domain can be used in vivo to deliver a chemically or
CD conformational rigidity to the peptides. The TSARs or comprising
CD biologically active molety, e9. metal ion, radioisotope, peptide, toxin
CD cenzyme, to the specific target or on the cell TPHy can also replace
CD cenzyme, to the specific target or on the cell TPHy can also replace
CD cenzyme, to the specific target or on the cell TPHy can also replace
CD cenzyme, to the specific target or on the cell TPHy can also replace
CD cenzyme, to the specific target or on the cell TPHy can also replace
CD cenzyme, to the specific target or on the cell TPHy can also replace
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                                        Q70469;
07-APR-1995 (first entry)
08-maric DNA sequence to generate a random TSAR peptide library,
TSAR; totally synthetic affinity reagent; synthetid; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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05-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            characterised and have designed activity allowing direct and rapid
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Pred. No. 1.03e-02;
27; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying proteins or peptide(s) which bind a ligand screening a recombinant vector library expressing fusion
                                                                                                                                                                                                                                                                         /note= "this sequence represents '2'; 2
sequence of 6,9 or 12 nucleotides (see
comments)"
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                          standard; DNA; 114 BP.
                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1993; US-013416,
30-DEC-1993; US-176500,
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKES DM, RAY BK;
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Matches 7: Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 gaatacacacggaagctacaagtgcttttgcctcagtggccacatgctcatgccagatgc 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                      /note= "this sequence represents '2'; 2 can be sequence of 6, 9 or 12 nucleotides (see comments)"
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Pred. No. 1.03e-02;
29; Mismatches 80; Indels
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/note= "encoded by 2"
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                                           Location/Qualifiers
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ID 070472 standard; DNA; 114 BP.
AC 070472;
DT 10-APR-1995 (first entry)
DE Generic DNA sequence to generat
KW TSAR; totally synthetic affinit
KW direct; rapid; detection; scree
OS Synthetic.
FF Key
FT Misc_feature 55..60
FT //tag= a
FT //reg= "encoded
                                                                                                                                                                             01 * ED 30-DEC-1993; US-1/0000
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
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ilarity 2.7%;
Conservative
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US-176500.
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Matches 3; Conser
                                                                                                                                                                                                                                                                 R65153
                                                       misc_feature
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                               Synthetic.
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identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins screening a binding domain and an effector domain bischosure; Page 36; 255pp; English.

Q70472 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides This generic formula can also be represented as follows: X(NNB)1(CAC)(NNB)11(CAC)(NNB)(CAC)(CAC)(NNB)2(NNB)6 - (CAC)(NNB)4. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. The peptides benerated by this and other generic sequences (Q70470-73) have invariant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     histidine residues incorporated into variant sequences. Takks are concatenated heterofunctional proteins or peptides, comprising at least two functional regions — a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The Takks or compens. comprising a Takk binding domain can be used in vivo to deliver a chemically or biologically active molety, e9. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, e9. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The Takks are easily characterised and have designed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 6 A; 12 C; 0 G; 0 T;
                                                                    01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKES DM. KAY BK;
                                                                                                                                                                                                         WPI; 94-279739/34.
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ö Length 114; // Match 8.4%; Score 25; DB 12; Length 114 Local Similarity 10.1%; Pred. No. 1.03e-02; nes 11; Conservative 24; Mismatches 74; Indels Query Match Best Loc Matches

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215 ccactgaggcaaaagcacttgtagcttccgtgtgtattcacacatctgtgttggcatggc 156 canbanbanbanbanbanbanbanbanbanbcacanbanbanbanban 65 9 g S

66 bnnbnnbnnbnnbcacnnbnnbnnbnnbcaccacnnbnnbnnb 114 셤

155 cggggtttcattccacactcattcacatcttgactgcaggttttcccgg 107

completed: Sat Apr 24 22:27:17 1999 Search

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

 n.a. database search, using Smith-Waterman algorithm n.a. Psrch_nn

Sat Apr 24 22:17:30 1999;

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MasPar time 484.95 Seconds 1107.807 Million cell updates/sec

Tabular output not generated.

>US-08-968-800-1 (1-300) from USO8968800.seq 299 Title:

1 ggctggagaagaaacagcaa.......atagctgtgaagacacagaa 300 ccgacctcttctttgtcgtt.......tatcgacacttctgtgtgtctt Description:
Perfect Score:
N.A. Sequence:
Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 Nmatch STD 2275026 seqs, 895388244 bases x 2 Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

embl-est56 Database:

1:em_estl 2:em_gssl 3:em_gss2 4:em_gss3 genbank-estl09 Database:

5:90b_est1 6:9b_est10 7:9b_est11 8:9b_est12 9:9b_est13 10:9b_est14 11:9b_est15 12:9b_est16 13:9b_est17 14:9b_est14 11:9b_est15 15:9b_est2 17:9b_est2 17:9b_est5 18:9b_est2 17:9b_est5 22:9b_est6 23:9b_est7 24:9b_est8 25:9b_est9 26:9b_gss1 27:9b_gss2 28:9b_gss3 29:9b_gss4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 9.757; Variance 1.776; scale 5.495 Statistics:

SUMMARIES

Pred. No.	1.05e-185	9.83e-62	8.07e-58	1.16e-40	5.67e-37	2.46e-33	4.91e-13	1.68e-11	1.68e-11	1.68e-11	1.68e-11	1.68e-11	1.54e-08
Description	ol34a06.sl Soares_NFL_	97SN1787 Rice Immature	97SN1787 Rice Immature	97SN1784 Rice Immature	97SN1784 Rice Immature	np48a02.s1 NCI_CGAP_Br	Homo sapiens ntcon2 co	ma05h07.rl Soares mous	me98d07.rl Soares mous	mille01.rl Soares mous	vh29c03.rl Soares mous	vn52d12.rl Barstead mo	Homo sapiens ntcon2 co
ID	AA913032	AA754459	AA754459	AA754458	AA754458	AA614649	AF034173	W09270	W82677	AA028399	AA497481	AA793395	AF034173
DB	18	12	12	12	12	10	11	σ	21	21	7	13	11
Query Match Length DB	420	252 12	252	247	247	334	2275	311	365	473	483	554	2275
Query Match	37.8	18.1	17.4	14.4	13.7	13.0	0.6	8.7	8.7	8.7	8.7	8.7	8.0
Score	113	54	52	43	41	39	27	26	26	26	56	56	24
ult No.	7	7	m	4	2	9	7	8	6	10	11	12	13
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.12e-07	.12e-0	.12e-0	.12e-0	.12e-0	.12e-0	.98e-0	.98e-0	.18e-0	.18e-0	.18e-0	.18e-	.18e-0	.18e-0	.18e-	.18e-0	.18e-	.18e-	.18e-0	.18e-0	.24e-	.24e-0	.24e-0	.24e-0	.24e-0	.24e-0	.24e-0	.24e-0	.24e-0	.24e-0	.24e-0		1998
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2d09.rl	1-fo-	R-C2p-	R-C0-9	10	85 Human	.s1	6	.0	yn48a04.rl H	EST32687 Emb	HS_2217_B2_F	mj50g04.rl S	ze14b12.rl S			r1	5pri	ρ,	b12.r1		h02.s1	.r1	s1	.81	.s1	3.81	sculu	11b04.s1	P-232	ם		EST
AA866946	5674	AI136687	AA963813	AA965236	W22070	T72162	T29884	M85706	H18256	AA329068	AQ178119	AA048871	W92242	N73094	AA991689	AA856482	AA698110	FR0029838	AA200492	T74911	13	8	N50973	2	8	8	34	8	AQ040342	3333	ALIGNMENTS	O MRNA
418 13	2 (2	5	54	57	80	36	2	56	72	91	86	36	73	77	96	47	98	04	07	9	9	47	26	98	7	99	83	14	44	23		420 bp
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23	23.7	53	23	23	23	22	22	21	21	21	21	21	21	21	21	21	21	21	21	20	20	20	20	20	20	20	20	20	20	20		1 8
	19	17	18	19	c 20	21	7	c 53	7	25	c 26	27	28	29	c 30	31	32	33	34	35	36	c 37	38	39	40	41	c 42	43	44	c 45		RESULT

	ol34a06.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1525330 3' similar to SW:FBN1_MOUSE Q61554 FIBRILLIN 1 PRECURSOR. ;, mRNA sequence.	AA913032	93052424	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Drimatos: Catarrhin; Dominidas; Dom	1 (bases 1 to 420)	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	Tumor Gene Index	Unpublished (1997)	Contact: Robert Strausberg, Ph.D.	Email: Robert Atranshergerih gov	This clone is available royalty-free through LLNL ; contact the	IMAGE Consortium (info@image.llnl.gov) for further information.	Insert Length: 1169 Std Error: 0.00	Seq primer: -40ml3 fwd. ET from Amersham	High quality sequence stop: 68.	Location/Qualifiers	14.0 /organisme"Homo capiens"	/ore="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with	a modified polylinker; Site_1: Not I; Site_2: Eco RI;	Equal amounts of plasmid DNA from three normalized	libraries (fetal lung NbHL19W, testis NHT, and B-cell	NCI_CGAP_GCBl) were mixed, and ss circles were made in	Victor following her purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver	was PCR-amplified cDNAs from pools of 5,000 clones made
RESULT 1 LOCUS	DEFINITION	ACCESSION	NID	SOURCE	ORGANISM		REFERENCE	AUTHORS	TITLE		JOURNAL COMMENT								FEATURES	source							

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA754459 252 bp mRNA EST 20-JAN-1998 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1787, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa
Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .252
//organism="Oryza sativa"
//organism="Oryza sativa"
//organism="Milyang23"
//note="Vector: PBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
//db_xref="taxon:4530"
//db_xref="taxon:4530"
from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711 and 729096-731399. Subtraction by Bento Abares and M. Fatina Bonaldo. "Abaref="taxon:9608" "Clone="imagE:152539" "Clone=lib="Soares.WFL_T_GBC_S1" | Ababast="DH108" | 98 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: myeun@sun20.asti.re.kr
Submitted by Back Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 252)
Mahn, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R., Moon, E.P.,
Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,
Lee, M.C. and Bun, M.Y.
                                                                                                                                                                                                                                                            110 GGGACAGTGTCAGCCTGTGTGCCAACCACGATGCAAACATGGTGAATGTATCGGGCCCAAA 169
                                                                                                                                                                                                                                                                                                                              170 CAAGTGCAAGTGTCATCCTGGTTATGCTGGAAAAACCTGTAATCAAGATCTAAATGAGTG 229
                                                                                                                                                                                                                                                                                                                                                                                                   230 TGGCCTGAAGCCCCGGCCCTGTAAGCACAGGTGCATGAACACTTACGGCAGCTACAAGTG 289
                                                                                                                                                                                                                                                                                                                                                                                                                        290 CTACTGTCTCAACGGATATATGCTCATGCCGGATGGTTCCTGCTCAAGTGCCCTGACCTG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 gggagtetgtgaagetacatgcgaacetggatgtaagtttggtgagtgcgtgggaceaaa 80
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                                                                                                                                                                                                       Length 420;
                                                                                                                                                                                                                                 0; Mismatches 79; Indels
                                                                                                                                                                                                Score 113; DB 18; I
Pred. No. 1.05e-185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          350 CTCCATGGCAAACTGTCAGTATGGCTGTGA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poales; Poaceae; Oryza.
                                                                                                                                                                                              Query Match
37.8%;
Best Local Similarity 70.7%;
Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Eun M.Y.
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                                                                                                                                                                                         Query Match
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                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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THORS
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JOURNAL
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                                                                                                                                                   ORIGIN
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/lab_host="E. coli Solm"
/lab_lost="E. 12 g 35 t 179 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa

Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;

Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;

Poales; Poaceae; Oryza.

(bases 1 to 252)

Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,

Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,

Lee,M.C. and Eun,M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA754459 252 bp mRNA EST 20-JAN-1998
978N1787 Rice Immature Seed Lambda ZAPII CDNA Library Oryza sativa
cDNa clone 978N1787, mRNA sequence.
AA754459
92801165
                                                                                                                                                                                                                                                                                         4
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/cultivar="Milyang23"
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Vector at 5'end with EcoRI and 3' end with Xho I site."
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/tissue_type="Immature Seed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 82 331 290 0301
Tel: 82 331 290 0307
Email: myeun@sun2O.asti.re.kr
Submitted by Back Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: Mi3 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                           STMTWGIVNWBNVSGDWHYWBVBNTKVDVGNHTRCSRWRBVTRMAHYHDYTNCBBYNNND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 catggcacatgtcctngagttcacacacgtagcatctggcatgagcatgtggc-cactga 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 YHMWHBBMYBBTGCMTCTMMCWBHYNTKCTASGWHTSTNYDVKSSTNTWGVTBSYDKSMH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GYWCSBBVKYHTKVSTTRATRSYTCVRKYCVMWMTKKVVKKYHVVBB-GCHBTDSKCKTM 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
                                                                                                                                                                                                                                                                                                                  1 HWDCTMNTVRGCCCCBAWMITSYBCHGNBVWVCVASHGNYMSVHNCTBRGTHCDCKNVNW 60
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: ::::::: | :: | :|::::|: :::::: ||:: :|:|:
90 tctgcatttgtttggtcccacgcactcaccaaacttacatccaggttcgcatgtagcttc
                                                                                                                                                                                                                              Length 252;
                                                                                                                                                                                                           18.1%; Score 54; DB 12; Length 252
Larity 13.0%; Pred. No. 9.83e-62;
Conservative 121; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
/clone="97SN1787"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                  Ouery Match
Best Local Similarity 1
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7

82

Query Match

Best Loc Matches

셤 ò 셤 ò

SASE COUNT

ORIGIN

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/crganism="Oryza sativa"
/crganism="Oryza sativa"
/cultivar="Milyang23"
/cultivar="Milyang23"
/note="Vector: pBluesript SK(+); Site_1: EcoRI; Site_2:
XhoT; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
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/clone="97$N1784"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA754458 247 bp mRNA EST 20-JAN-1998
97SN1784 Rice Immature Seed Lambda ZAPII CDNA Library Oryza sativa
cDNA clone 97SN1784, mRNA sequence.
AA754458
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Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
National Inst. of Agri. Sci. and Tech, RDA
National Inst. of Agri. Sci. and Tech, RDA
Tel. 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 247)
Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
Kim,W.Y., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
Unpublished (1998)
                                                                                                                                    260 catgiccingagitcacacacgitagcatiggcatgagcatgiggcc-actgaggcaaaa 202
                                                                                                                                                                                                    HCRYIVBWYYARSKYGYGTBYYSWNVDINTGGTGVGKTTVNVHSGWNNRCSNSVVYVWBT 120
                                                                                                                                                                                                                                                                     201 geactigtagetteegtgtgtatteacacatetgtgttggeatggeeggggttteattee 142
                                                                                                                                                                                                                                                                                                                                     121 AYCDYBHYBDRANHVDDTRCTNDRGYCNYTASDNGTSATKRVTGYDKTDSDCGGGCWRKV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 WNDCSDNAHCRYTVBWYYARSKYGYGTBYYSWNVDTNTGGTGVGKTTVNVHSGWNNRCSN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 SVVYVWBTAYCDYBHYBDRANHVDDTRCTNDRGYCNYTASDNGTSATKRVTGYDKTDSDC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 agtotgtgaagotacatgogaacotg-gatgtaagtttggtgagtgogtgggaccaaaca 82
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 TYGSSBYBRCGVNVWVRTTSMWTDKSTKM-BSMDMSRRSRVHYGRWMBNKKRGMSRNW 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24
                                                                                                                                                                                                                                                                                                                                                                       1 HWDCTMNTVWRGCCCCBAWMNKHTHMMTBBWCCVRRVGTTTNNGKHNGRTTTWNDCSDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 gtttggtcccacgcactcaccaaacttacatccaggttcgcatgtagcttcacagact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
          Indels
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          Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87; Mismatches
          98;
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Similarity 10.1%;
18; Conservative
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Eun M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa
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Matches 18; Conser
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      37;
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JOURNAL
COMMENT
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                                                                                                                                                                                                           61
          Matches
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*Not; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
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Bibryophyta: Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
1 (bases 1 to 247)
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Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seg primer: M13 Reverse Primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           87 VDVGNHTRCSRWRBVTRMAHYHDYTNCBBYNNNDYHWWHBBMYBBTGCMTCTMWCWBHYN 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JAN-1998
                                                                                                                                                                                                                                                                                                                                                   27 GNBVWVCVASHGNYMSVHNCTBRGTHCDCKNVNWSTMTWGTVNWBNVSGDWHYWBVBNTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 TKCTASGWHTSTNYDVKSSTNTWGVTBSYDKSMHGYWCSBBVKYHTKVSTTRATRSYTCV
                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 247;
                                                                                                                                                                      Length 252;
                                                                          179 others
                                                                                                                                                                         Score 52; DB 12; Length 252
Pred. No. 8.07e-58;
104; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Immature Seed"
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/lab_host="E. coli SOLM:
16 c 21 g 34 t 169 ot)
days after pollination" coli SOLR" 12 g 35 t 179 ot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 12;
Pred. No. 1.16e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97SN1784 Rice Immature Seed Lambda SCDNA clone 97SN1784, mRNA sequence. AA754458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .247
/organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 atacacacggaagctacaagtgcttttgcct 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKYCVMWMTKKVVKKYHVVBBGCHBTDSKCK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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      /dev_stage="5
/lab_host="E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.4%;
                                                                                                                                                                            17.4%;
12.8%;
                                                                          21 c
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                                                                                                                                                                                                    Local Similarity
les 27; Conserv
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LOCUS DEFINITION

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KEYWORDS

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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

FEATURES

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human.
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//organism="Nemo sapiens"
//organism="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                     raco14649 334 bp mRNA EST 16-OCT-1997 np48a02.s1 NCI_CGAP_Br1.1 Homo sapiens cDNA clone IMAGE:1129514, AA614649
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 334)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
173 GGGCWRKVTYGSSBYBRCGVNVMVRTTSMWTDKSTKWBSMDMSRRSRVHYGRWMBNKK 230
                                                                                                           144 ITCCIACCITGATTACAGGITITTCCAGCATAACCAGGATGACATTGGACTTGTTTGGC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 318.
Location/Qualifiers
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Pred. No. 2.46e-33;
0; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
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Best Local Similarity 68.98;
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                       human.
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Bases I to 311)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
 2275 bp mRNA EST 22-DEC-1997 ntcon2 contig mRNA, partial sequence, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MU9270 311 bp mRNA EST 01-OCT-1997 ma05h07.rl Scares mouse p3NMF19.5 Mus musculus cDNA clone 303709 protein precursor; mRNA sequence.
                                                                                                                         Eukaryotas, Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 2275)
Tripodis,N. and Ragoussis,J.
Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1476 AAMWRYKRWKRRKGRRKRMTGMYKRMYRAMMAMCAMMACWWYYWKMRGHKKCWKYRKYK 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 aacacagatgtgtgaatacacaggaagctacaaagtgctttgcctcagtggccacatgc 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 27; DB 11;
Pred. No. 4.91e-13
50; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /map-"optl.3"
/clone-"ntcon2 contig"
/tissue_type-"liver; brain"
/dev_stage="fetus"
/note-"similar to Br140"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1536 KYTSTYYKSWSRWYWYTTYTYWYCWCCTSMKSAS 1569
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Local Similarity 10.6%;
hes 10; Conservative
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                 Homo sapiens
AF034173
                                                                                                              Homo sapiens
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Mus musculus
AF034173
                                                        92707735
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Murinae; Mus.

1 (bases 1 to 473)

Marta, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA028399 473 bp mRNA EST 16-AUG-1996 milled).rl Scares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 464184 5' similar to SN:TLD_DROME P25723 DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR; ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Vector: pT7T3D-Pac (Pharmacia) with a modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 atgccaacacagatgtgtgaatacacacggaagctacaagtgcttttgcctcagtggc 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 ATGCCAGCAAGACTGTGTGAACACGTTCGGCAGCTACGAGTGTCAGTGCCGCAGTGGC
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                               /clone="403597"

/clone_lib="Soares mouse p3NMF19.5"

/dev_stage="19.5 dpc total fetus"

/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 26; DB 21; Lei
Pred. No. 1.68e-11;
0; Mismatches 16;
      Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 353.
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High quality sequence stop: 462.
Location/Qualifiers
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                                                                                         /organism="Mus musculus"
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                                             Location/Qualifiers
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Best Local Similarity 72.4%;
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BASE COUNT
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                                                                                                                                                                                                                                                  W82677 365 bp mRNA EST 12-SEP-1996 me98d07.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone 403597 5' similar to gb:M22488 BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Unpublished (1996)
On Sep 13, 1996 this sequence version replaced gi:1393691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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0
                                                                                                          MGI: 200469
Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="303709"
/clone="11b="soares mouse p3NMF19.5"
/clone_lib="soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
a 82 c 88 g 62 t
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Pred. No. 1.68e-11;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                     /organism="Mus musculus"
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                                                                                                                                                                     quality sequence stop: 290.
Location/Qualifiers
                                                                                                                                                  Seq primer: mob.REGA+ET
High quality sequence s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 72.4%;
42; Conservative
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Best Local Similarity
Matches 42; Conserv
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AA497481 483 bp mRNA EST 01-JUL-1997 vh29c03.rl Scares mouse mammary gland NbMMG Mus musculus cDNA clone 876868 5' similar to SN:BMP1_MOUSE P98063 BONE MORPHOGENETIC AA497481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
/note="Organ: mammary gland; Vector: pI7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I
oligo(dI) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="464184"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
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WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                   Score 26; DB 21; Length 473;
Pred. No. 1.68e-11;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                            /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 420.
Location/Qualifiers
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                                                                                                                                                                                                                                                  /sex="unknown"
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Best Local Similarity 72.4%;
Matches 42; Conservative
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a 126 c
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KEYWORDS

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FEATURES

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T 3']; double-stranded CDNA was lighted to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library Constructed and normalized by Bento Soares and M.Fatima Bonaldo."
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 554) Musica, Mus. Mustra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Rucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Tan, F., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vn52di2.rl Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone 1024823 5' similar to gb:M22488 BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (HUMAN);, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                             /clone_lib="Soares mouse mammary gland NbMMG" /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                            Score 26; DB 7; Length 483;
Pred. No. 1.68e-11;
0; Mismatches 16; Indels
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High quality sequence stop: 475.
Location/Qualifiers
1. .554
                                                                                                                                                                                                                                     /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
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                                                                                                                                                    /db_xref="taxon:10090"
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The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                             130 g
                                                                                                                                                                           /clone="876868
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Best Local Similarity 72.4%;
Matches 42; Conservative
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92856350
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases I to 418)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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     house mouse.
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2 (bases 1 to 2275)
Tripodis, N. and Ragoussis, J.
Direct Submission
Submitted (13-NOV-1997) Division of Medical and Molecular Genetics,
Guy's Hospital, 7th floor, Guy's Tower, London SE1 9RT, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA866946 418 bp mRNA EST 16-MAR-1998
N424099.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
1023857 5', mRNA sequence.
AA866946
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                                                                                                                                                                                                                                                                                                                                                                     AF034173 2275 bp mRNA EST 22-DEC-1997
Homo sapiens ntcon2 contig mRNA, partial sequence, mRNA sequence.
AF034173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens Bukaryotae; Metazoa: Chordata; Vertebrata; Mammalia; Butheria; Bukaryotae; Catarrhin1; Hominidae; Homo.

1 (bases 1 to 2275)
Tripodis,N. and Ragoussis,J.
Tripodis,N. and Ragoussis,J.
Generation of a transcription map in the region immediately entromeric to human MHC across the 6p21.2-6p21.3 chromosomal
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   myotubes and producing
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rapidly, forming contractile myotubes and p
characteristic muscle proteins."
/db_xrsf="texon:10090"
/clone="1024823"
/clone="1024823"
/clone="1024823"
/clone="1024823"
/clone="1024823"
/clone="102482"
/clone="102482"
/clone="102482"
/clone="102482"
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                                                                                                                                                                                            Length 554;
                                                                                                                                                                                            Score 26; DB 12; Length 554
Pred. No. 1.68e-11;
0; Mismatches 16; Indels
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Pred. No. 1.54e-08;
52; Mismatches 29; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="liver; brain"
/dev_stage="fetus"
/note="similar to Br140"
619 c 470 g 599 t
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
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Best Local Similarity 13.5%;
Matches 13; Conservative
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Best Local Similarity 72.4%;
Matches 42; Conservative
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/note="organ: Skin; Vector: pBluescript SK-; Site_1:
BCORI: Site_2: XhoI: Cloned unidirectionally Primer:
Oligo dT: Whole skin from Il week old C5PBL/6 female mice.
Average insert size: 1.0 kb; Unit.ZAP XR Vector: -5,
adaptor sequence: 5' GAATTCGGCACGAC 3' -3' adaptor
/db_xref="taxon:10090"
/clone="1023857"
/clone="lib="Stratagene mouse skin (#937313)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human clone=201021 primer=M13RP1 library=Soares fetal liver spleen
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                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:574633
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yq69b11.rl Homo sapiens cDNA clone 201021 5' similar to
SP:FBN1_HUMAN P35555 FIBRILLIN 1 ;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 GACTGCAGGTAATCCCACCGGACCCTGGAAGTCATCTCCATTCATGTGG 343
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Pred. No. 4.12e-07;
0; Mismatches 13; Indels
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/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
| 91 c 116 g 89 t
                                                                                                                                                                                                                                                                                                                  Seq primer: -28ml3 revl ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"/strain="C57BL/6"
The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 388.
Location/Qualiflers
1. .418
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Best Local Similarity 73.5%;
Matches 36; Conservative
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Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 326
Source: ImAGE Consortium, LLNL
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further information.
Deuterostomia: Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Anniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 446)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M.; Kucaba,T., Le,M., Lennon,G., Marra,M., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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/organism="Homo sapiens"
/clone="201021"
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8 a 93 c 104 g 107
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                                                                                                                                                       Wilson,R.
The WashU-Merck EST Project
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n.a. - n.a. database search, using Smith-Waterman algorithm Psrch_nn Thu Apr 29 03:05:32 1999; MasPar time 2494.84 Seconds 1525.983 Million cell updates/sec no or

Tabular output not generated.

>US-08-968-800-2 (1-1611) from USO8968800.seq 1607 Description:
Perfect Score:
N.A. Sequence:
Comp: Title:

1 ggctggagaagaaacagcaa......aattactagctgaaaaattg 1611 ccgacctcttctttgtcgtt......ttaatgatcgactttttaac

Dbase 0; Query 0 Nmatch STD

TABLE default Gap 6

Scoring table:

602357 seqs, 1181590623 bases x 2 Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in 7:em_pa 8:em_or 9:em_or 10:em_pat 11:em_ph 12:em_pl 13:em_ro 14:em_un 15:em_vi genbank110
16:gb_ba1 17:gb_ba2 18:gb_htg 19:gb_in 20:gb_om 21:gb_or 22:gb_pat 23:gb_ph 24:gb_pl1 25:gb_pl2 26:gb_pr1 27:gb_pr2 28:gb_pr3 29:gb_ro 30:gb_st 31:gb_sts 32:gb_sy 33:gb_un 34:gb_vi Database:

Mean 11.423; Variance 5.514; scale 2.072 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Re	Result No.	Score	Query Match	Query Match Length DB	DB	OI.	Description	Pred. No.
່ ບ	;	108	6.7	7218	22	166494	Sequence 14 from paten	1.81e-60
O	7	41	2.6	215	22	128278	Sequence 5 from patent	1.24e-09
	٣	37	2.3	2070	13	AF051401	Caenorhabditis elegans	4.99e-07
	4	37	2.3	2139	13	AF051402	Caenorhabditis elegans	4.99e-07
U	S	37	2.3	10772	13	AF012089	Drosophila melanogaste	4.99e-07
	ø	35	2.2	7218	22	I66494	Sequence 14 from paten	9.13e-06
	7	36	2.2	9662	26	HUMFIBRLLN	Homo sapiens fibrillin	2.15e-06
	80	36	2.5	9940	56	HSFIBRMR	H. sapiens mRNA for fib	2.15e-06
	σ	35	2.5	10772	13	AF012089	Drosophila melanogaste	9.13e-06
O	10	36	2.2	74371	27	AC005369	Homo sapiens chromosom	2.15e-06
	11	33	2.1	2156	56	HSFIBUC	H.sapiens mRNA for fib	1.56e-04
	12	33	2.1	2349	56	HSFIBUA	H.sapiens mRNA for fib	1.56e-04
	13	33	2.1	2359	56	U01244	Human fibulin-1D mRNA,	1.56e-04

\$25 26 HSFIBUB H.sapiens mRNA for fib 1.56e-0 \$30 29 MMU22493 Mus musculus fibrillin 6.25e-0 \$724 29 AF007248 Mus musculus mutant fi 6.25e-0 \$25 32 MUSFBNIA Mouse fibrillin (Fbn-1 6.25e-0 \$15 22 128278 Sequence 5 from patent 9.42e-0 \$65 22 AR024229 Sequence 22 from patent 9.42e-0 \$61 26 HUMCLNIN Human calnexin mRNA, c 2.45e-0 \$188 26 HUMCLNIER Human calnexin mRNA, c 2.45e-0 \$181 26 HUMCLNIER Human calnexin mRNA, c 2.45e-0	117 26 HUMIP90 Homo sapiens integral 2.45e- 371 27 AC005369 Homo sapiens chromosom 9.42e- 55 22 AR024229 Homo sapiens chromosom 9.42e- 55 22 AR024229 Sequence 22 from paten 3.53e- 558 21 AF051400 Gallus gallus fibulin 3.53e- 578 21 AF051399 Gallus gallus fibulin 3.53e- 578 21 AF051399 Gallus gallus fibulin 3.53e- 578 21 AF027596 Danio rerio tolloid mR 3.53e- 578 29 MMENACT MOUSE mRNA for nidogen 3.53e- 578 29 MMENACT MOUSE mRNA for entacti 3.53e- 578 29 MMESPAZ Human fibrillin 3.53e-	117 20 H50004787 Human LIDILILIT 2 HINNA 5:358-0 321 27 HVAC004787 Homo sapiens Chromosom 5:38-0 342 4 GWNGMIG SOYbean Ngm-16 gene co 1:298-0 352 26 HSFIB5 H. Sapiens MRNA for fib 1:298-0 350 20 BOVXAAAA GASDIENS MRNA, COMPI 1:298-0 351 9 CELCSEG CASONTABADILIS slegans 4.608-0 351 10 AC00513 Homo sapiens chromosom 4.608-0 351 18 AC002553 Homo sapiens chromosom 1:298-0 351 18 322945 Human DNA sequence *** 4.608-0 351 17 AC005187 Homo sapiens Chromosom 4.608-0 351 18 18 4.532945 Human DNA sequence *** 4.608-0
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ALIGNMENTS

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Rhabditina; Rhabditoidea; Secernentea; Rhabditia; Rhabditida;
1 (bases I to 2070)
Barth, J.L., Argraves, K.M., Roark, E.F., Little, C.D. and
Argraves, W.S.
Isolation of chicken and nematode fibulin-1 homologs and
Unpublished
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                                                    851 ttcccttttttacctccatgagagttcccgcctctggaaactatctttcatagttgaag 792
                                                                                                        791 ggctgcaagttcaccttaggggtaggagtcctggtggggttctgggggtaacatttttaatt 732
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Bennett,A., Labaritch,J.M., Powell,A. and Stotz,H.
Plant inhight sof fungal polygalacturonases and their use to control fungal disease
Patent: US 5569830-A 5 29-OCT-1996,
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Pred. No. 1.24e-09;
82; Mismatches 91; Indels
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91819054
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Best Local Similarity 16.3%;
Matches 34; Conservative
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DLLNNNEPCVAPVGFSAGCLRSFNKCCNGDIEITHASEIITGRPLNDPHVLHGGBRCA
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FKCIFTLSGGTGYAMDSETERCRDVDECNLGSHDCGPLYQCRNTDGSYRCDAKGGDG
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DECITRAGRYCDLCABCINTIGSFECKCRPGFQLASDGRRCEDYNBCTTGTAACEDY
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GYKLQPDGRTCYDVDDGSGSDRVCWNTLGSFCKHSIDCPTNYINHSLNKNOIA
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NLDYYQQRHFRIVQDENIGIYQLKRFISGPTVETIKVNIHTKSRTGVILAFNBAIIEI
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Barth, J.L., Argraves, K.M., Roark, E.F., Little, C.D. and Argraves, W.S.
Isolation of chicken and nematode fibulin-1 homologs and characterization of the nematode fibulin-1 gene
                                                                                                                                                                                                                                                                                                                     /map="between elt-1 and daf-10"
/note="partial sequence obtained from EST clone ykllb1"
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precursor (FBLN1) mRNA,
                                                                                                                                                          S_{C}^{S}
2 (bases 1 to 2070)
Barth,J.L., Argraves,K.M., Roark,E.F., Little,C.D. and Argraves,W.S.

Argraves,W.S.

Direct Submission
Submitted (26-FEB-1998) Cell Biology and Anatomy, Medical
University of South Carolina, 171 Ashley Avenue, Charleston,
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Pred. No. 4.99e-07;
0; Mismatches 42; Indels
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    .2070
    /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
    /chromosome="IV"

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Best Local Similarity 65.3%;
Matches 79; Conservative
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ECCIKRAGHVCDLSAECINTIGSFECKRPPGPLASDGKRCEDVNECTTGIAACBDV
VNI PGSYQCICUPGFALGPDGTKCEDIDECSIWAGSGNDLCWGGCINTKGSLOCOFP
GYKIQPSQCICUPGGAGDFACKEDIDECSIWAGSGNDLCWGGCINTKGSLKCQCP
GYKIQPSGTCVDDGFALGPDGTKCEDIDECSIWAGSGNCOVILGSFKCHSIDCPTNI HIDSLIKNRCN
RQPSAGGLPEECSKVPLFLTYQFISLARAVPISSHRRAITLFKVSAPNHADTEVNFEL
OLKTIVGAPENCIAPALGARKRNSAVYTLRDSLDGPQTVKLQLLLRMSKKGK
NFNTZWANLIVDVAAHRRHNYHPPLMKIR
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SSHCEHLCHDRGEBKVECCRGGRDAPDGAACVDIDECATLMDDCLESORCLNTPGS
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ELQNPWTGECTSITCPNGYTPRNGMCNDIDECVTGHNCGAGEECVNTPGSFRCQDKG
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Drosophila melanogaster cysteine proteinase-1 (CP1) gene, complete
cds, and phenylalanyl tRNA synthetase gene, partial cds.
AF012089
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P-element-induced recombination in Drosophila melanogaster: hybrid
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/note="partial sequence obtained from EST clone ykllb1"
                 Argraves, W.S.
Direct Submission
Submitted (26-FEB-1998) Cell Biology and Anatomy, Medical
University of South Carolina, 171 Ashley Avenue, Charleston, SC
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Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
1 (bases 4546 to 4553)
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Barth, J.L., Argraves, K.M., Roark, E.F., Little, C.D. and
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/db_xref="taxon:6239"
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97132596
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/product="cysteine proteinase-1"
/db_xref="PID:92305221"
/db_xref="PID:92305221"
/translation="MRTAVLLPLIALLAVQAVSFADVVMEEWHTFKLEHRKNYQDET
EERFRILSTENENKHKIAKHNORFAEGKVSFKLAVNKYADLLHHEFRQLMNGFNYTLHK
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HFRKSGVLVSLSEQNLVDCSTKYGNNGCNGGLMDNAFRYIKDNGGIDTEKSYPYEAID
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EPQCDAQNLDHGVLVVGFGTDESGEDYWLVKNSWGTTWGDKGFIKMLRNKENQCGIAS
ASSYPLV"
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SSWTKPNSPATRRAVKLMEHEMKHVLVGLTKDLFGPRIKYRWVDTYFPFTQPSWELEI
YFKDNWLEVLGGGIMRHEILQRSGVHQSIGYAFGVGLERLAMVLFDIPDIRLFWSNDS
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/db_xref="PID:92305222"
/translation="MLLTLRVQGARHWLKSTRCLASSAAPAKSPSSPPQLEVSGSTYA
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PVVTVQQNFDNLLI PADHVSRQKSDCYY INQQHLLRAHTTAHQVELI SGGLDNFLVVG
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DMVEQISLVDKFKHPKTGKSSVCFRIVYRHMERTLTQAEVNEIHKQIASASVDSFNVQ
                                                                                                                                                                                           University
                                                                                                                     3 (bases 1 to 10772)
Gray, Y.H.M., Sved.J.A., Preston,C.R. and Engels,W.R.
Direct Submission
Submitted (30-JUN-1997) School of Biological Sciences, Universi
of Sydney, Biology Al2, Sydney University, NSW 2006, Australia
Location/Qualifiers
Structure of the cysteine proteinase (CP1) gene of Drosophila melanogaster and associated mutational effects

"Dnpublished"
                                                                                                                                                                                                                                                                  /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
join(872. 1000,2310. 2426,6476. 6690,6751. 7707)
/gene="CP1"
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join(8110. .9300,9370. .>9532)
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Pred. No. 4.99e-07;
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/gene="CP1"
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/gene="CP1"
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/gene="CP1"
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/gene="CP1"
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                                                                     1759 KMWNTRTWARMAWASWARWKWKTSAAAAYSAWRKMWKWWAYRAMKKTWMWAAWKWRWKAA 1818
                                    501 tatacagtcatatcgtccactgatatattgcagttcgaaaccaatgtgacatttgcagta 442
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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83; Mismatches 54; Indels
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Dorner,F., Schaiflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers
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     Mismatches 46;
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Hum. Mol. Genet. 2, 961-968 (1993)
93372860
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166494
92724471
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/db_xref="taxon:9606"
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1491 c 1486 q.
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                                                                                                                    /db_xref="PID:g306746"
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HKLNEVSQKCEDIDECSTIPGICEGGECTNIVSSYFCKCPPGFYISPDGIRCIDVRPG
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MVIPGRPEYPPPLGPIPPVLPVPPGFPPGPQIPVPRPPVEYIKPSREPPRVLDVNVT
DYCQLVRYLCQNGRCIPTPGSYRCECNKGFQLDLRGECIDVDECEKNPCAGGECINNQ
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DECEEGKHDCTEKQMECKNLIGTYMCICGPGYQRRPDGEGCVDENECQTKPGICENGR
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EPDVCKHGQCINTDGSYRCECPFGYTLAGNECVDTDECSVGNPCGNGTCKNVIGGFFC
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LQISSTPLYKKKELNOLEDKYDKDKYLSGELGDNLKMKIQVLLH"
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/standard_name="Marfan syndrome gene"
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2234 c
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9741
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Similarity 66.4%;
73; Conservative
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REALOGGAAADRAPCAPECAPELLIMUGE INTRREKLLET ALGFTVILLASTTSHCADAN
REALOGGAAADRAPCAPECGGSENDILLET ALGFTVILLASTTSHCADAN
SCGDGFCSRPWACCTCPSGGAEDALKGPWCGSRYNYCCPGWKTLPGGWCGVTVPICKH
SCGDGFCSRPWACCTCPSGGAEDALKGPWCGSCSDHCLCOKGY 1GTHC
GOPVCESGCLNGGRCWAPRCACTYGFTGPCBRYTATGACODVDECQLSGTV
GONTOCSFCKCKPAGHKLNEVSGKCEDIDECSTPFGFTVISOPPCCAPEGCTV
CINTYGCATYGRAWGHPCEWCPAGPHPCRRETIPNTTGACODVDECQLSGTV
CINTYGCSFCKCKPAGHKLNEVSGKCEDIDECSTPFGFTVVSSTFCKCPPGF
YTSPDGTRCTIDVRPGYTALINGRCSNOLPGSTRWCCCOLAGRWSPGVTVAPEMC
TYSPDGTRCTIDVRPGYTALINGRCSNOLPGSTFRWCCCOLAGRWSPGVTVAPEMC
YTSRDTRCTPGTRCTTOWRCSNOLPGSTRWCCOLAGRWSPGTDLINGRETIPNDE
CENRPCAGGECINNGRCSTRYCORAGYOSTLTRTECEDIDECGGECTNNGRCINTDG
SFHCVCNAGFHYTRDCKNCEDDDECSTSTRWCLNGRCINTDG
SFHCVCNAGFHYTRDCKNCEDIDECESPCINGRCVDINGRCINTDG
KTCLIFTRETPGTTKRDLKNCEDIDECESPCINGRCVDINGRCYNGGCRN
TPGSSPYCTCPKGGTTKRDLKNCEDIDECESPCINGRNCSPCINGRG
YSRIKGTOCEDIDECESPCINGRATINGATIKSGFKCOCPSGMTLAGTGETCHPT
TKEITINGRAPFILIAGRHRWAACCCSVGAAMGTBECGESCPRRRYFEYELLCHPTET
CFLRYEDEGCTIPAGRCHRWAACCCSVGAAMGTBECGESCPRRRYFEYELECTORTET
TKEITINGRAPFENISACIDIDECESPCRATIGESTRATILDIDECTORTET
TKEITINGRAPFENISACIDIDECESPCRATIGESTRATILDIDECTORTET
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TKEITINGRAPFENISACIDIDECESPCRATIGESTRATILDIDECTORTET
TRESTRYCTORTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fibrillin binds calcium and is coded by CDNAs that reveal a multidomain structure and alternatively spliced exons at the 5' end genomics 17 (2), 476-484 (1993)
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ICDGGQCTNIPGEYRCLCYDGFMASEDMKTCVDVNECDLNPNICLSGTCENTKGSFIC
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EPSSGCSGHDWEQPPPPPRESEPPLLHWQGPPEVGAAPGEGGRSPARGTGGGTAGPRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDECSNGTHMCSQHADCKNTMGSYRCLCKEGYTGDGFTCTDLDECSENLNLCGNGQCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (19-DEC-1991) C.L. Maslen, Oregon Health Sciences Univ, Dept of Mol and Medical Genetics, 3181 S W Sam Jackson Pk Rd, Portland Oregon 97201, USA
3 (bases 1 to 9940)
                              17-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                        Partial sequence of a candidate gene for the Marfan syndrome Nature 352 (6333), 334-337 (1991)
                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corson, G.M., Chalberg, S.C., Dietz, H.C., Charbonneau, N.L. and
                                                                                                                                                                                                                                                                                                                              Maslen, C.L., Corson, G.M., Maddox, B.K., Glanville, R.W. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Sep 3, 1993 this sequence version replaced gi:31412. Location/Qualifiers
                                 PRI
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/db_xref="PID:e81922"
/db_xref="PID:q1335064"
/db_xref="SWISS-PROT:P35555"
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...srlbRMR 9940 bp RNA
H.saptens mRNA for fibrillin.
X63556 X62010
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                                                                                                                       g397553
fibrillin.
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

(Cases 4546 to 453)
Gray, Y. H., Tanaka, M.M. and Sved, J.A.
P-element-induced recombination in Drosophila melanogaster: hybrid YCYAKFEGGKCSSPKSRNHSKQECCCALKGEGWGDPCELCPTEPDEAFRQICPYGSGI Submitted (30-JUN-1997) School of Biological Sciences, University of Sydney, Biology Al2, Sydney University, NSW 2006, Australia ö 502 gatataaatgaatgtactatggatagccatacgtgcagccaccatgccaattgcttcaat 561 Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R. Structure of the cysteine proteinase (CP1) gene of Drosophila melanogaster and associated mutational effects Gaps ö 4542 ACCATGGGATCTTACCGCTGTCTGTGCAAGGAAGGATACACAGGTGATGG 4591 /note="either G or T in various cDNA clones" /note="either C or T in various cDNA clones" Gray,Y.H.M., Sved,J.A., Preston,C.R. and Engels,W.R. Direct Submission Length 9940; 2 others 0; Mismatches 37; Indels Score 36; DB 26; Pred. No. 2.15e-06; 2422 t Genetics 144 (4), 1601-1610 (1996) 97132596

9

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DNA PRI 01-AUG-1998
5, BAC clone 119j3 (LBNL H175), complete
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 74371)
Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Kadner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M., Sojeski,H., Subramanian,S. and Martin,C.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   % (bases 1 to 74371)
Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Bavis,C.A., Kadner,K., Miguel,T., Pitluck,S., Pollard,M., Direct Submission
Submitted (01-AUG-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157, Sequence submitted by:
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join(3246. .3410,3721. .3828)

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Location/Qualifiers
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7113. .7373
                                                                                                                                                                                                                                   Homo sapiens
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553 tgcttcaat 561
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                                                                                                                                             sequence.
AC005369
g3367505
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AUTHORS
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                SOURCE
                                 ò
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ASSYPLV"
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/ COCUM_S-L-L-L

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/ Canslation="MiltleNOGARHWIKSTRCIASSAAPAKSPSSPQLEVSGSTVA

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                               oin(872. .1000,2310. .2426,6476. .6690,6751. .7707)
gene="CP1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1752 WWAYAWMKMWWTRTWARMAMASWARWKWKTSAAAAYSAWRKMWKWWAYRAWKKTWWWAW 1811
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Pred. No. 9.13e-06;
62; Mismatches 47; Indels
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                  'db_xref-"taxon:7227
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Best Local Similarity 15.5%;
Matches 20; Conservative
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à a ŏ

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36901. 37164
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complement(34021 .34144)
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27774. .28057
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28040. .28066
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                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 2156)

Korenberg, J.R., Chen, X.N., Tran, H. and Argraves, W.S.

Localization of the human gene for fibulin-1 (FBLN1) to chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'translation="MERAAPSRRVPLPLLLLGGLALLAAGVDADVLLEACCADGHRMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEEGFFTTRKVSPHSGVVALTKPVPEPRDLLLTVKMDLSRHGTVSSFVAKLFIFVSAE
                                                                                                                                                                                                                          Direct Submission
Submitted (03-JUL-1990) Argraves W.S., American Red Cross, 15601
Crabbs Branch Way, Rockville, MD 20855, USA
2 (bases 1 to 2156)
Argraves,W.S., Tran,H., Burgess,W.H. and Dickerson,K.
Fibulin is an extracellular matrix and plasma glycoprotein with repeated domain structure
J. Cell Biol. 111 (6 Pt 2), 3155-3164 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1526 CAGTGCAGCTGCCCCTCGTCTGGCTACAGGCTGGCCCCCAATGGCCGCAACTGCCAAGAC 1585
                               21-AUG-1995
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2156)
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Pred. No. 1.56e-04;
0; Mismatches 34; Indels
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Cytogenet. Cell Genet. 68 (3-4), 192-193 (1995)
95145011
                           PRI
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    2156
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         H.Sapiens mRNA for fibulin-1 C. X53743
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2156
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                                                                                       fibulin-1 C; glycoprotein.
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Matches 67; Conservative
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3 (bases 1 to 2349)
Korenberg, J.R., Chen, X.N., Tran, H. and Argraves, W.S.
Localization of the human gene for fibulin-1 (FBLN1) to chromosome band 22q13.3
Cytogenet. Cell Genet. 68 (3-4), 192-193 (1995)
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TDKILEVEEEQEDPYLNDRCRGGPCKQQCRDTGDEVVCSCFVGYQLLSDGVSCEDVN
ECITGSHSCRLGESCINTVGSFRCQRDSSCGTGYELTEDNSCKDIDECESGIHNCLPD
FICQNTLGSFRCRPKLQCKSGFIQDALGNCIDINECLSISAPCPIGHTCINTEGSYTC
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ISRMCVDVNECQRYPGRLCGHKCENTLGSYLCSCSVGFRLSVDGRSCEDINEGSSSPC
SQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGHICSYRCINIPGSFQCS
CPSSGYRLAPNGRNCODIDECVTGIHNCSINETCFNIQGAFRCLAFECPENYRRSAAT
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THORDCSLPYATESKECRMVQEQCCHSQLEELHCATGISLANEQDRCATPHGDNASLE
                                                                                                                                                                                                   Argraves, W.S.

Argraves, W.S.

Submission

Submitted (103-JUL-1990) Argraves W.S., American Red Cross, 15601

Crabbs Branch Way, Rockville, MD 20855, USA

2 (bases 1 to 2349)

Argraves, W.S., Tran, H., Burgess, W.H. and Dickerson, K.

Fibulin is an extracellular matrix and plasma glycoprotein with J. Cell Biol. 111 (6 Pt 2), 3155-3164 (1990)
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                              21-AUG-1995
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2349)
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Pred. No. 1.56e-04;
0; Mismatches 34; Indels 0;
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/db_xref="taxon:9606"
/tissue_type="placenta"
//chromosome="22q13.3"
             H.Sapiens mRNA for fibulin-1 A.
X53741
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evidence=experimental
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/db_xref="PID:931415"
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/product-"fibulin-1 A"
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/codon_start=1
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2 (bases 1 to 9830)
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Best Local Similarity 66.3%;
Matches 67; Conservative
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/translation="MERAAPSRRVPLPLLLLGGLALLAAGVDADVLLEACCADGHRMA
/translation="MERAAPSRRVPLPLLLLGGLALLAAGVDADVLLEACCADGHRMA
THORDCSLPYATESKECRNVQBOCCHSQLEEBHCATG15LANEQDRCAPPHGDNASLE
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TDKIIEBYEEBQEDPYLNDRCRGGGPCKQOCRPTGDEVYCSCFWGYQLLSDGVSCEDVN
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OKNUPPRIGEOTYHLINEEGTREVVDVDECAPAEPCRGKGHRCVNDSRGSFREEKTGYTFDG
ISRMCYDVNCCORFPCENTLGSFLCSCSVGFRLSVDGRSCEDINESSSSPC
SQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDBCALPTGGHICSFRCINIPGSFQCS
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LQQEKTDTVRCIKSCRNDVVTCYFDVYHTISHTVISLPTFREFTRPEETIFLRALTPP
HPASQANIIFDITEGRIRDSFDIIKRYMDGMTVGVVRQVRPIVGFFHAVLKLEMNYVV
GGVVSHRNVVNNTIFVSETWF"
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2 (bases 1 to 2525)
Argraves,W.S., Tran,H., Burgess,W.H. and Dickerson,K. Fibulin is an extracellular matrix and plasma glycoprotein with repeated domain structure
                                                                                                                                                                                                                                                            Direct Submission
Submitted (10-SEP-1993) S. Argraves, Biochemistry, American Red
Cross, 15601 Crabbs Branch Way, Rockville MD 20855 USA
Location/Qualifiers
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2359)
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2525)
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Pred. No. 1.56e-04;
0; Mismatches 34; Indels
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   Human fibulin-1D mRNA, complete cds.
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/db_xref="taxon:9606"
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fibulin-1 B; glycoprotein.
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/db_xref="gW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ECITGSHSCRLGESCINTVGSFRCQRDSSCGTGVELTEDNSCKDIDECESGIHNCLPD
GROWTLGSFRCRPKLDCKSGF1QDALGNCIDINECLSISPOPIGHTCINTEGSSYC
GRWVPNCGRCYHLNEGTRCVDRJCAGNCIDINECLSSFRCECKTGYFPG
ISRMCYDVNECGRCYHLNEGTRCWCDFILSSYLCSCSVGFRLSVDGRSSSPC
ISRMCYDVNECQRYGHCGHKCDENTLGSYLCSCSVGFRLSVDGRSCEDINECSSSPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQECANVIGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGHICSYRCINIPGSFQCS
CPSSGYRLAPNGRNCQDIDECVTGINNCSINETCFNIQGAFRCLAFECPENYRRSAAT
                                                                                                                                                                                   Korehberg, J.R., Chen, X.N., Tran, H. and Argraves, W.S. Localization of the human gene for fibulin-1 (FBLN1) to chromosome and 22q13.3 Cytogenet. Cell Genet. 68 (3-4), 192-193 (1995) 95145011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (13-MAR-1995) Yashpal S. Kanwar, Northwestern University Medical School, Pathology, 303 E. Chicago Ave., Chicago, IL 60611,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murinae; Mus.
1 (bases 1 to 9830)
Ota,K., Kumar,A., Wada,J., Liu,Z. and Kanwar,Y.S.
Molecular cloning of mouse fibrillin-1 and its role in the renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1526 CAGTGCAGCTGCCCCTCGTCTGGCTACAGGCTGGCCCCCAATGGCCGCAACTGCCAAGAC 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 cagtgcctgtgtccatcctcaggactccgcctggccccaaatggaagagactgtctagat 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-1995
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Mus musculus fibrilin-1 (Fbn1) mRNA, complete cds.
022493
9726323
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Pred. No. 1.56e-04;
0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QKSKKGRQNTPAGSSKEDCRVLPWKQGLEDTHLDA"
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J. Cell Biol. 111 (6 Pt 2), 3155-3164 (1990)
91100426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370 attgatgaatgtgcctctggtaaagtcatctgtccctacaa 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="placenta"
1. .2525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="fibulin-1 B" 2525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           736 g
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                                                                                                                                                                                                                                                                                          PSGQISPSCGSRSIQHOSIRCMNGGSCSDDHCLCQKGYIGTHCGOPVCESGCLNGGRC
VAPNRCACTYGFTGPQCERDYRTGPCFTVVSNQMCQGQLSGIVCTKTLCCATYGRAWG
HPCEMCPAQPHPCRRGFIPNIRTGACQDVDECQAIPGMCQGGNCINTVGSFECKCPAG
                                                                                                                                                                                                                                                                                                                                           HKFNEYSOKCEDIDECSTIPGVCDGGECTNTVSSYFCKCPPGFYTSPDGTRCVDVRPG
YCYTALANGRCSNQLPQSITKMQCCCDLGRCWSPGVTVAPEMCPIRSTEDFNKLCSVP
                                                                                                                                                                                                                                                                                                                                                                              LVIPGRPEYPPPPIGPLPPVQPVPPGYPPGPVIPVPRPPPEYPYPSPSREPPRVLPFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECTCEEGREPGPMMTCEDINECAQNPLLCAFRCVNTYGSYECKCPVGYVLREDRRMCK DEDECARGKHOCTEKOMECKNLIGTYMCICGFGYQRRPDGEGCIDENECQTKPGICEN GRCLNTLGSYTCECNDGFTASPTQDECLDNREGYCFSEVLQNMCQIGSSNRNPYTKSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCDGGRGWGPHCEICPFEGTVATKKLCPHGRGFMTNGADIDECKVIHDVCRNGECVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKGVCONTPGSTTCECCRGFSLDOSGASCEDVDECEGNIRCOHGONIIGGYRGSCPO
GYLQHYOWNOCVDENECLSAHVCGGASCHNTLGSYKCMCPTGFOYEQFSGGCQDINEC
GSSQAPCSYGCSNTEGGYLCGCPPGYFRIGQGHCVSGWGMGRGPEPPASSEMDNSL
SPEACYECKINGYPKRCRKRRSTNETDASDIQDGSEMEANVSLASWDVEKPASFAKNI
SHVNNKYRILEELLPALTTLANHNRYLIESGNEDGFFKINQKEGVSYLHFTKKKPVAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRGSYHCICKTGYTPDITGTACVDLNECNQAPKPCNFICKNTEGSYQCSCPKGYILQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGRSCKDLDECATKQHNCQFLCVNTIGGFTCKCPPGFTQHHTACIDNNECTSDINLCG
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/clone_lib="cDNA library made by our group"
/tissue_type="kidney"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSLOISSTPLYKKKELNQLEDRYKDYLSGELGDNLKMKIQILLH
2371 c 2665 g 2292 t
                                                                                                                                                                                                                                                                          RGGGGHDALKGPNVCGSRYNAYCCPGWKTLPGGNQCIVPI
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                                                                                                                                                                            220. .8841
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                 source
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FEATURES
                                                                                                                                                                     CDS
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Gaps ö Query Match 2.0%; Score 32; DB 29; Length 9830; Best Local Similarity 63.8%; Pred. No. 6.25e-04; Matches 74; Conservative 0; Mismatches 42; Indels

ORIGIN

4306 TGCACAGATCTGGATGAATGCTCTAATGGAACCCACATGTGCAGCCAACACGGGGACTGC 4365

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Search completed: Thu Apr 29 03:47:27 1999 Job time : 2515 secs.

Generic DNA sequence Generic DNA sequence Generic DNA sequence Generic DNA sequence

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***************************************	, = = = = = = = = = = = = = = = = = = =	(TA)	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	"Psrch_nn n.a n.a. database search, using Smith-Waterman algorithm	In on: Sat Apr 24 23:15:27 1999; MasPar time 264.82 Seconds 827.661 Million cell updates/sec Tabular output not generated.	Title: >US-08-968-800-2 Description: (1-1611) from US08968800.seq Perfect Score: 1607 N.A. Sequence: 1 ggctggagaagaaacagcaaaattactagctgaaaaattg 1611 Comp: ccgacctcttctttgtcgttttaatgatcgacttttaac	Scoring table: TABLE default Gap 6

1. 79e-04 2. 20e-03 2. 20e-03 2. 20e-03 2. 20e-03 2. 52e-03 2. 52e

070470 070470 070473 070472 070476 070460 070460 070461

cDNA encoding human r Encodes truncated hum Encodes thrombomoduli

cDNA encoding a human Encodes thrombomoduli Soluble thrombomoduli Thrombin-binding subs

Encodes thrombomoduli Recombinant thrombin-Human thrombomodulin

Human endothelin-l an Generic DNA sequence Generic DNA sequence Generic DNA sequence Generic DNA sequence Human endothelin ETA DNA encoding cell pro DNA encoding cell pro Elmeria tenella genom DC43 TSAR library gen Generic DNA sequence Human interleukin 8 a Sequence encoding thr Sequence encoding thr Sequence encoding thr Sequence encoding thr

ALIGNMENTS

n-geneseq32 l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part24 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38

188442 seqs, 68026449 bases x Minimum Match 0% Listing first 45 summaries

Post-processing:

Database

Searched:

STD

Nmatch

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description

DB

Length

Query Match]

Result No.

Mean 9.403; Variance 5.340; scale 1.761

Statistics:

fragment encodi

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vhsyyvvhvvshhhsvhhvvhvhhvhvvhvhvhvhyhvyvsvctcaaqcctcgg 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shank DD, Spers PA;
WPI; 93-378844/48.
New oligo:nucleotide probes specific for Mycobacteria - used
detection and amplification of Mycobacteria nucleic acid in
samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                              751746 standard; cDNA; 91 BP.
051746;
31-MAY-1994 (first entry)
011gonuclectide probe MK14-A
011gonuclectide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 9; Length 91;
Pred. No. 2.86e-10;
41; Mismatches 10; Indels
                                                                                                                                                                                                                                                   ss.
Synthetic.
EP-571911-A.
01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1993; US-889651.
(BECT ) BECTON DICKINSON CO.
Shank DD, Spears PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.6%;
Similarity 16:4%;
10; Conservative
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279
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2.86e-10 7.10e-11 3.70e-06 3.70e-06 1.36e-05 1.36e-05

Oligonucleotide probe
Oligonucleotide probe
Base substituted E.co
Base substituted E.co
Generic DNA sequence
Generic DNA sequence
Generic DNA sequence
Fibulin C.
Fibulin A.
Fibulin B.
Generic DNA sequence

QS1746 QS1746 QS1746 NN81164 NN070467 Q70465 Q70469 Q101008 Q11008 Q11008 Q1008 Q1008

0 0 0 0 0

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108 Others;

11 T;

17 G;

47 C;

21 A;

204 BP;

Sequence

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Introducing random point mutations into nucleic acods -

by prepn of single stranded template, annealing a primer, elongation,

misincorporation, completion of molecules and screening.

Disclosure; p; English.

Random point mutations were introduced into the alpha fragment of

E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligomucleotide was hybridised to possible nucleotide positions within a specified region. The variable 3' ends aperated in this way are used as primers for transcriptase and the molecules are misincorporated by the amplified and then expressed in a suitable host-vector system.

The sequence covers all 176 difft base substitutions, most of which center and any given mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
(Q51735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection.
See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-NoV-1990 (first entry)

Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 gssvhsyyvvhvvshhhsvhhvvhhvhvsvvvvhhvvhvvhr-vhyhvyvsvct 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ĥ
                                                                           Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-1988.
30-MAR-1988; 105163.
03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P. Knowles J. Koivula A. Bamford J. Reinikainen T;
WPI: 88-279927/40.
                                                                                                                                                                                                                                         new origo:nucleotide probes specific for Mycobacteria - usedetection and amplification of Mycobacteria nucleic acid in samples
                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 9; Leus...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19..69
/*tag- a
/function=multiple cloning site
187..204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                       EP-571911-A.
01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
Shank DD, Spears PA;
                                         31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
             Q51746 standard; cDNA; 91 BP. Q51746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N81164 standard; DNA; 204 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                    larity 5.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     2.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= b
                                                                                                                                                                                                           Spears PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                     WPI; 93-378844/48
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                                                                                                            Synthetic
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RESULT
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Throaducing random point mutations into nucleic acods -

Introducing random point mutations into nucleic acods -

Py prepn of single stranded template, annealing a primer, elongation,

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Random point mutations were introduced into the alpha fragment of

E.coli beta galactosidase. The wild type sequence was obtained as a

it to generate a popn of DNA molecules which terminate at all

possible nucleotide positions within a specified region. The

variable 3' ends generated in this way are used as primers for

reverse transcriptase and the molecules are completed to forms that can be

The sequence covers all 176 difft base substitutions, most of which

Secured singularly in any given mutant.
                                                                  97 mrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvhnhnncncccb 156
                                                                                     1325 ttctcccatgccagggcattgttactgttttcacaaaacactcgaagtttcccgacttg 1266
                                               Gaps
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070467 standard; DNA; 114 BP.
070467 standard; DNA; 114 BP.
05-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker;
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N81164;
08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions;
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03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
WPI; 88-279927/40.
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          Length 204;
                                      51; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 1; Length 204;
Pred. No. 2.86e-10;
57; Mismatches 42; Indels
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     Score 42; DB 1; L
Pred. No. 7.10e-11;
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/*tag= a
/function=multiple cloning site
187..204
                                                                                                                                   157 nnhvchnvhbnnhrnwayvrhdarrddvhccvch 190
                                                                                                                                                             717 gaaaaagagagaaaaattaaaaaatgttaccca 750
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Ouery Match 2.6%;
Best Local Similarity 10.6%;
Matches 10; Conservative
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Matches 12: Conco
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(UYNC-) UNIV
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31-JAN-1994;
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                                                                                                                 Fowlkes DM,
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P-PSDB;
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O70467 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)12. X and Y are flanking restriction sites (X is not the same as Y) that are cond specified further. Other generic sequences are shown in R65151-54. TSARs are concatenated by these generic sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins or peptides. Comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains The oligonucleotides are also designed so
                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rightity to the peptides. The TSARS or compsns. comprising a TSAR binding domain can be used in vivo to radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eq. menoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing
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Pred. No. 3.70e-06;
33; Mismatches 71; Indels
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/note= "this sequence represents '2'; 2 o
sequence of 6, 9 or 12 nucleotides (see
                                                                       Z , Z,
                                                                      s sequence represents 'Z'; Z
6, 9 or 12 nucleotides (see
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                            Location/Qualifiers
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/*tag= a
/note= "this s
sequence of 6,
comments)"
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Q70468 standard; DNA; 114 BP.
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Similarity 1.9%;
2; Conservative
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US-176500.
US-189331.
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P-PSDB; R65153.
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Seguence 114 BP;
direct; rapid;
Synthetic.
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31-JAN-1994;
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Trenuis rounding proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins promprising a binding domain and an effector domain bisclosure; Page 35; 255pp; English .

Disclosure; Page 35; 255pp; English .

Comprising a peneric DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides This generic formula can also be represented as follows: X(NNB)12(TGC)(NNB)7(TGC)(NNB)10V. X and Y are flanking restriction sites (X is not the same as Y) that are cont specified further. Other agencies are shown in 707466-68.

Conterspecified further. Other agencies generic sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker of finity for a ligand and a second effector peptide portion that is chart the expressed peptide contains? The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in or flanking, the unpredicted or variant residues. The TSARs or comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, caldisotope, peptide, toxin or enzyme, to the specific target or on the contour person of hybridoma for mointen or notivity or notivity may also replace the function of macromolecules, eg. morellity or polyclonal antibodies and therefore circumvent the need of corrometry and or polyclonal antibodies and therefore circumvent the need of corrometry or notivity or nordiversion and activity or antibody artivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
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Pred. No. 3.70e-06;
33; Mismatches 75; Indels
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/note= "this sequence represents '2'; Z
sequence of 6, 9 or 12 nucleotides (see
comments)"
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Similarity 3.6%;
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05-APR-1995 (first entry)
comments)"
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US-176500.
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WPI: 94-27939/34.

Provikes DW, Kay BK:

Provikes DW, Way BK:

Provikes DW, PR TSAR BK
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070469;
070469;
07-1995 (first entry)
Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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/note= "this sequence represents 'Z'; Z can be
sequence of 6,9 or 12 nucleotides (see
comments)*
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Pred. No. 3.70e-06;
33; Mismatches 75; Indels
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UNIV NORTH CAROLINA.
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UNC-) UNIV NORTH CAROLINA.
FOWIKES DM. KAY BK;
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Best Local Similarity 3.6%;
Matches 4; Conservative
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01-FEB-1994;
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CC (70469 is a generic DNA sequence used to generate random TSAR peptide
This generic formula can be represented as follows: X(TGC)(NNB)10-
CC (TGC)(NNB)2(TGC)(NNB)14(TGC)Y. A and Y are flanking restriction
sites (X is not the same as Y) that are not specified further. This
csites (X is not the same as Y) that are cloverleaf in structure. Other
CC generic sequences are shown in 070465-68. Other specific peptides
CC generic sequences are shown in R65150-54. TSARS are
CC concatenated beterofunctional proteins or peptides, comprising at least
two functional regions - a binding domain with affinity for a ligand and
a second effector peptide portion that is chemically or biologically
CC a second effector peptide portion that is chemically or biologically
CC ontains 2 or 4 cysteine residues positioned in, or flanking, the
CC ontains 2 or 4 cysteine residues positioned in, or flanking, the
CC onformational rigidity to the peptides. The TSARS or compons. Comprising
CC offormational rigidity to the peptides. The TSARS or compons.
CC offormational rigidity to the peptides. The TSARS or compons.
CC offormation of macromolecules, eg. menoclonal or polyclonal antibodies
CC of enzyme, to the specific target or on the cell. They can also replace
CC offormation of macromolecules, eg. menoclonal or polyclonal antibodies
CC demarion or in vivo antibody production. The TSARS are easily
CC characterised and have designed activity allowing direct and rapid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 gcnnbanbanbanbanbanbanbanbanbanbtgcnnbanbanbanbanbannann 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purified fibilin, DNA encoding it and antibodies reactive with it useful as diagnostic and therapeutic component.
Claim 10; Fig 3; 56pp; English.
The fibulin c CDNA was sequenced from a clone isolated from lambda gill human placental CDNA library using a polyclonal antiserum.
The three forms (A, B and C) are identical from their 5, ends to a divergence point at posn. 1707, after which they are distinct through to the poly(A) tail. The CDNA can be used to express
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 nbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbt 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beta-1 integrin; adhesion; receptor; fibronectin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.36e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 12;
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/label= point of divergence
2126. 2131
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G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
98..2059
/*tag= b
/product= fibulin C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection in a screening process. Sequence 114 BP; 0 A; 4 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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011010 standard; cDNA; 2200 BP.
011010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 5.4%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAY-1991 (first entry) Fibulin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LJOL-) LA JOLLA CANCER REG
(AMMA-) AMER NAT RED CROSS.
Ruoslahti El, Argraves WS;
WPI; 91-087250/12.
N-PSDB; R11150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-AUG-1990; U04662
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NPI: 91-087250/12.

NPI: 91-087250/12.

NPI: 91-087250/12.

NPI: 91-087250/12.

NPI: 91-087250/12.

NPI: 91-087250/12.

The claim 10, Fig 3; 56pp; English.

Claim 10, Fig 3; 56pp; English.

The fibulin A cDNA was sequenced from a clone isolated from lambda gtll human placental cDNA library using a polyclonal antiserum.

Claim 10, Fig 3; 56pp; English.

Claim 10, Fig 4; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1526 cagtgcagctgccctcgtctggctacaggctggccccaatggccgcaactgccaagac 1585
                                                                                                                                                                                                                                                                                                                                                                                                    310 cagtgcctgtgtccatcctcaggactccgcctggccccaaatggaagagactgtctagat 369
                                                                                                                                                                                                                                                                                                  0; Gaps
recombinant fibulin in a host cell. Fibulin binds to the vytoplasmic domain of the betal subunit of integrin adhesion receptors in a cation-dependent, EDTA-reversible manner. It can be used to manipulate adhesion of cells to fibronectin, collagen,
                                                                                                       laminin, and possibly also other proteins. Antibodies reactive with the protein have important diagnostic and therapeutic uses. See also 011008 and 011009.

Sequence 2200 BP, 464 A, 654 C, 647 G, 435 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laminin, and possibly also other proteins. Antibodies reactive with the protein have important diagnostic and therapeutic uses. We also 011009 and 011010. Sequence 2355 BP: 526 A; 668 C; 682 G; 479 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                           Length 2200;
                                                                                                                                                                                                                                                                                               0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta-1 integrin; adhesion; receptor; fibronectin; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                        attgatgagtgtgtgactggcatccacaactgctccatcaa 1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 attgatgaatgtgcctctggtaaagtcatctgtccctacaa 410
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Larity 66.3%; Pred. No. 1.36e-05;
Conservative 0; Mismatches 34
                                                                                                                                                                                                                                           Score 33; DB 2; I
Pred. No. 1.36e-05;
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/label= point of divergence
2286..2291
/*tag= d
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98..1708
/*tag= b
/product= fibulin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q11008 standard; cDNA; 2355
Q11008;
21-MAY-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAR-1991.
17-AUG-1990; U04662.
18-AUG-1989; US-395773.
(LJOL.) LA JOLLA CANCER RES.
(AMNA-) AMER NAT RED CROSS.
                                                                                                                                                                                                                                           7 Match 2.1%;
Local Similarity 66.3%;
nes 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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                                                                                                                                                                                                                                           Query Match
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- useful as diagnostic and therapeutic component.

Claim 10; Fig 4; 56pp; English.

C The fibulin BoDNA was sequenced from a clone isolated from lambda gtil human placental CDNA library using a polyclonal antiserum.

C divergence point at posn. 170; after which they are distinct through to the poly(A) tail. The CDNA can be used to express recombinant fibulin in a host cell. Fibulin binds to the cytoplasmic domain of the betal subunit of integrin adhesion creceptors in a cation-dependent, EDNA-reversible manner. It can be used to manipulate adhesion of cells to fibronectin, collagen, laminin, and possibly also other proteins. Antibodies reactive with the protein have important diagnostic and therapeutic uses.

See also 011008 and 011010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cagtgcagctgccctcgtctggctacaggctggccccaatggccgcaactgccaagac 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 cagtgcctgtgtccatcctcaggactccgcctggccccaaatggaagagactgtctagat 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G5-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concatenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purified fibulin, DNA encoding it and antibodies reactive with it
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Pred. No. 1.36e-05;
0; Mismatches 34; Indels
                                                                                                                                                       Beta-1 integrin; adhesion; receptor; fibronectin; ss.
of divergence
                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                            98..1813
/*tag= b
/product= fibulin B
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/label= point c
2505..2510
                                                                                            BP
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Q70465 standard; DNA; 114 BP.
Q70465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1%; 3
larity 66.3%; 1
Conservative
                                                                              T 11
Q11009 standard; cDNA; 2555
                                                                                                                                                                                                                                                                                                                                                                                                                     (LJOL-) LA JOLLA CANCER RES (AMNA-) AMER NAT RED CROSS.
                                                                                                                       21-MAY-1991 (first entry)
Fibulin B.
                                                                                                                                                                                                                    /*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruoslahti EI, Argraves WS;
WPI; 91-087250/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 67; Conser
                                                                                                                                                                                                    signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; R11149
                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                    mat_peptide
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1586
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Upschosure, Page 35; 255pp; English.

O70465 is a generic DNA Sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides This generic formula can also be represented as follows: X(NNB)6(TGC)(NNB)11Z(NNB)4(TGC)(NNB)3Y. X and Y are flanking restriction sites (X is not the same as Y) that are Conterpresented by these generic sequences are shown in 70746668.

CC OMPERISTOR THE CONCATENDATE GENERAL SEQUENCES ARE SHOWN IN COMPISSING ALL TEARS are concatenated heterofunctional proteins or peptides, affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker chemically or biologically active. They may further comprise a linker chemically or biologically active. They may further comprise a linker confer some degree of confine or variant residues. These residues for that the expressed peptide contains 2 or 4 cysteine residues positioned confer some degree of conformational righdity to the peptides. The TSARs celliver a chemically or biologically active molety, eg. metal ion, or flanking, the unpredicted or variant residues. These residues celliver a chemically or biologically active molety, eg. metal ion, or adioisotope, peptide, toxin or enzyme, to the specific target or on the monoclonal or polyclonal antibodies and therefore circumvent the need conformation are polyclonal antibodies and therefore circumvent the need conformation are polyclonal antibodies and therefore circumvent the need production. The TSARs are easily characterised and have designed containty allowing direct and rapid detection in a screening process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1038 tatctcggttgactgcagcttcaatcatgggatctgtgactggaaacaggatagagaa 1097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generic DNA sequence to generate a random TSAR-9 petide library.
TSAR: totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
Synthetic: rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                          Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain proteins pisclosure; Page 35; 255pp; English.
                                                                ಹ
                                                            can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/note= "this sequence represents 'z'; z can
sequence of 6, 9 or 12 nucleotides (see
comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 114;
      55..60
/*tag= a
/note= "this sequence represents '2'; z
sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32; DB 12; Length 114;
Pred. No. 4.97e-05;
32; Mismatches 76; Indels
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                                                                                                                                                                                                (UVNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JT 13
Q70466 standard; DNA; 114 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.0%;
larity 3.6%;
Conservative
                                                                                         comments)"
                                                                                                                                                                                                                                                                                 P-PSDB; R65150 and R65151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q70466;
05-APR-1995 (first entry)
                                                                                                                                                                     US-013416.
US-176500.
                                                                                                                                                                                                                                                                 WPI; 94-279739/34.
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Best Local Similarity
      misc_feature
                                                                                                                                                                                     30-DEC-1993;
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Terebula Konsia.

Identifying proteins or peptide(s) which bind a ligand - by
Screening a recombinant vector library expressing fusion proteins

PT screening a recombinant vector library expressing fusion proteins

PT comprising a binding domain and an effector domain

CG 70466 is a generic DNA sequence used to generate random TSAR (Totally

Synthetic Affinity Reagents) peptides. This generic formula can also be

CC PAT and Y are flanking restriction sites (X is not the same as Y)

CC TOTAGE 68. Other specific peptides generated by these generic sequences

CC TOTAGE 68. Other specific peptides generated by these generic sequences

CC TOTAGE 68. Other specific peptides generated by these generic sequences

CC TOTAGE 68. Other specific peptides generated by these generic sequences

CC TOTAGE 68. Other specific peptides generated by these generic sequences

CC TOTAGE 68. Other SPECIFIC PROPER AGENTICATION OF THE STATE AGENT OF THE AGENT OF 
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P-PSDB: R58378.
Identifying proteins or peptide(s) which bind a ligand - by
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Pred. No. 4.97e-05;
30; Mismatches 70; Indels
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                                                                                                     31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA
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Q70470 standard; DNA; 114 BP.
Q70470;
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5.7%;
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31-JAN-1994; US-189331.
(UINC-) UNIV NORTH CAROLINA.
FOWIKES DM, KAY BK;
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P-PSDB; R65152.
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represented as follows: X(NNB)4(CAC)(NNB)4(CAC)(NNB)8Z(NNB)6(CAC)(NNB)8 -(CAC)2(NNB)Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. The peptides generated by this and other generic sequences (070471-73) have invariant histidine residues incorporated into variant sequences. TSARs are concatenated
                                                                                                                                                                                                                                                                                                               heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The TSARs or compaiss a 18AR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rappid detection in a screening process. Sequence 114 BP; 5 A; 10 C; 0 G; 0 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain

Disclosure; Page 36: 255pp: English.

Q70473 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(CAC)(NNB)2(CAC)(NNB)2(CAC)(NNB)2(CAC)(NNB)2(CAC)(NNB)2(CAC)(NNB)2(CAC)(NNB)3(CAC)(NNB)3(CAC)(NNB)3(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(CAC)(NNB)4(
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                              comprising a binding domain and an effector domain
Disclosure; Pageg 36; 255pp; English.
Q70470 is a generic DNA sequence used to generate random TSAR (Totally
Synthetic Affinity Reagents) peptides. This generic formula can also be
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expressing fusion proteins
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Pred. No. 1.79e-04;
28; Mismatches 68; Indels
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   vector library
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30-DEC-1993; US-176500.
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(UYNC.) UNIV NORTH CAROLINA.
FOWIKES DM, KAY BK;
WPI: 94-279739/34.
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Q70473 standard; DNA; 114 BP.
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Best Local Similarity 6.8%;
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Generic DNA sequence to gen
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affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The TSARs or composes. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily
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                                                                                                                                                                                                                                                                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 11.687; Variance 2.100; scale 5.565 Statistics:

l:em_est1 2:em_gss1 3:em_gss2 4:em_gss3
3:enbank-est109
5:gb_est1 6:gb_est10 7:gb_est11 8:gb_est12 9:gb_est13
10:gb_est14 11:qb_est15 12:gb_est16 13:qb_est17
14:gb_est18 15:gb_est19 16:gb_est2 17:gb_est20
18:gb_est2 19:gb_est3 20:gb_est4 21:gb_est5 22:gb_est6
23:gb_est7 24:gb_est8 25:gb_est9 26:gb_gss1 27:gb_gss2
28:gb_gss3 29:gb_gss4

2275026 seqs, 895388244 bases x

Minimum Match 0% Listing first 45 summaries

Post-processing:

Searched:

embl-est56

Database: Database:

SUMMARIES

	Score	Ouery Match I	Match Length DB	DB	Ω	Description		Pred. No.
Т	555	34.5	626	9	AA195615	zr37b10.r1	Soares NhHM	0.00e+00
8	451	28.1	208	21	AA025649	ze85d03.rl	Soares feta	0.00e+00
m	438	27.3	472	9	AA436507	zv08c07.rl	Soares NhHM	0.00e+00
4	398	24.8	446	16	R99817	yq69b11.r1	Homo sapien	0.00e+00
Ŋ	355	22.1	473	19	R76984	y166d08.rl	Homo sapien	
9	353	22.0	411	16	R64051	y122c04.rl	Homo sapien	0.00e+00
7	354	22.0	454	16	H03936	y144a05.s1	Homo sapien	0.00e+00
· œ	332	20.7	429	22	AA009900	ze83d06.rl	Soares feta	0.00e+00
6	331	20.6	341	16	R68291	y106a03.rl	Homo sapien	0.00e+00
10	311	19.4	442	Ŋ	T65608	yc76b01.rl	Homo sapien	0.00e+00
c 11	296	18.4	406	18	AI057064	oz07b04.x1	Soares_feta	0.00e+00
12	285	17.7	344	21	W80921	zd90b04.rl	Soares feta	0.00e+00
13	277	17.2	347	ß	R11377	yf42e08.rl	Homo sapien	0.00e+00

yh64e08.rI Homo sapien 0.00e+00 yh46e02.rI Homo sapien 0.00e+00 yh48e12.rI Homo sapien 0.00e+00 yh48e12.rI Homo sapien 0.00e+00 yh53d04.rI Homo sapien 0.00e+00 yh57f04.sI Homo sapien 0.00e+00 yh57f04.sI Homo sapien 0.00e+00 yh57f04.sI Homo sapien 0.00e+00 yh58f10.rI Homo sapien 0.00e+00 yw65a12.rI Homo sapien 0.00e+00 zj29e09.sI Soares feta 2.90e+179 ox13h06.sI Soares feta 2.90e+179 ow69c06.sI Soares feta 2.06e+119 ze85d03.sI Soares feta 1.06e+10 ze85d03.sI Soares feta 1.06e+10 yx57N1787 Rice Immature 1.96e-74 yr57N1787 Rice Immature 1.96e-74 yr57N1784 Rice Immature 1.96e-74 yr57N1784 Rice Immature 1.90e-34 yr57N1784 Rice Immature 1.80e-36 ruman placenta cDNA 5' 7.85e-18 yi40f0.rI Homo sapien 7.85e-18 yi50q07.rI Homo sapien 7.85e-18	MENTS SI Homo sapiens cDNA clone 665563 5', mRNA sl Homo sapiens cDNA clone 665563 5', mRNA heria; Primates; Catarrhini; Hominidae; heria; Primates; Catarrhini; Hominidae; hachar., Leb.M., Lemnon,G., Marra,M., hlfing,T., Ten.F., Trevaskis,E., A., Wohldmann,P. and Wilson,R. A., Wohldmann,P. and Wilson,R. Soll of Medicine Box 8501, St. Louis, MO 63108 du cyalty-free through LLNL; contact the age.llnl; gov) for further information. I Error: 0.00 pp: 477. sapiens" xed (see below); Vector: pT773D-Pac
R27678 R27153 R27153 R24466 R27428 R22182 R22182 R24180 R32182 C17012 R34484 R3977654 AA913032 AA025548 AA734459 AA734459 AA734458 AA734458 AA734458 AA734458 AA734458 AA734458 RA734649 R22137 R22137 R22137 R26676 R71008 R71008 R71008 R71008	IGN Pu m Pu k Ru Ku Ku Ku Ku Ku Ku Ku Ku Ku
3374 3564 3561 3561 3561 3561 37551 37551 37561 37561 3757 3757 3757 3757 3757 3757 3757 375	626 bp mR 626 bp
22122222222222222222222222222222222222	AA195615 sequence. AA195615 EST. AA195615 EST. human. Human. Humon saplens bukeryotae; 19 Wertebrata; Homo. Hiller,L., Hallman,M., H Parsons,J., Waterston,R. WashG-Merck Wash
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Normalized libraries (melanocyte 2NDHM, pregnant uterus NDHPU, and fetal heart NDHH19W) were mixed, and ss circles were made in vitro. Following RAP purification, this DNA reaction. The driver was PCR-amplified cDNAs from pools 5,000 clones made from the same 3 libraries. The pools 340488-345479, and 484488-489479. "Albraries." The pools //clone="665563"
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                                                                                                            /clone_lib="Soares NhHMPu S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
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8
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Pred. No. 0.00e+00;
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ilarity 97.1%;
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Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the Seq primer: -28M13 rev2 from Amersham
IMAGE Consortium (info@lange.llnl; gov) for further information.

Seq primer: -28M13 rev2 from Amersham
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Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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/dev_stage="19 weeks"
/lab_host-"DH10B (ampicillin resistant)"
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/clone_lib="Soares fetal heart NDHH19W"
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508 bp mRNA EST 14-AUG-1996 Soares fetal heart NbHH19W Homo sapiens cDNA clone

AA025649 508 bp ml 2e85d03.rl Soares fetal he 365765 5', mRNA sequence. AA025649

DEFINITION

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/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI: Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHW, pregnant uterus
NDHPU, and fetal heart NDHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               rial eukaryotes; Metazoa; Chordata;
Eutheria; Primates; Catarrhini; Hominidae;
                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 441.
                                                                                                                               tggcaggtcacatgaaagacattggccgattgaaacttctcctacctgacctgcaacccc 1222
1045 gttgactgcagcttcaatcatgggatctgtgactggaaacaggatagagaagatgatttt 1104
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                                                                                               361 TGNAAGGTCACAAGAAAGACATTGGCCGATTGAAACTTCTCCTACCTGACCTGCAACCCC
                                 GACTGGAATCCTGCCTGATCGAGATAATGCTATTGGCTTCTATATTGGCAGTTCCGGCCT
                                                                                                                                                               421 CAAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGAAGNACAAAGTCGGGNAACT
                                                                                                                 Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/tissue_type="Pooled human me]
pregnant uterus"
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Vertebrata; Mammalia; Eut
                                                                                                                                                                                                                                TCGAGTGTTTGTGAAAAACAGTACCA
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human clone=201021 primer=M13RP1 library-Soares fetal liver spleen
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 446)
Hillier, Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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                                                Gaps
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                                                                                            3 AGCTICAATCAIGGGATCIGIGACTGGAAACAGGATAGAGAAGATGAITTTGACTGGAAT
                                                                                                                                                                                         63 CCTGCTGATCGAGATAATGCTATTGGCTTCTATATGGCAGTTCCGGCCTTGCGAG-TCAC
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Score 438; DB 6; Le
Pred. No. 0.00e+00;
0; Mismatches 9;
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WashU-Merck EST Project
Washington University School of Medicine
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Query Match 27.3%;
Best Local Similarity 97.5%;
Matches 461; Conservative
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                                  Email: est@watson.wustl.edu
High quality sequence stops: 326
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
                                                                                                                                                                                                                                                                                                                            121 AGATGTGTGAACACATTTGGAAGCTACTACTGCAAATGTCACATTGGTTTCGAACTGCAA 180
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Y166008.rl Homo sapiens CDNA clone 144207 5'
9851616
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Pred. No. 0.00e+00;
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Parkway, Box 8501,
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/organism="Homo sapiens"
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ilarity 97.1%;
Conservative
4444 Forest Park F
Tel: 314 286 1800
Fax: 314 286 1810
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Best Local Similarity
Matches 433; Conserv
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BASE COUNT
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WashU-Merck EST Project
WashU-Merck EST Project
WashU-Merck EST Project
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 358
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 TATGICCAGAIAGCCITITAICTGIGGAIGACTGAAIGTIACIAICTITAIAITTGACTT 299
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        I (bases 1 to 473)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 11; Indels 1; Gaps
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Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo
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78 c 1
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96.8%;
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I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library Homo sapiens
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                                                                          Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
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1 (bases 1 to 411)
Hilliar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Pred. No. 0.00e+00;
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4444 Forest Park Parkway, Box 8501,
Tel: 314 286 1800
Fax: 314 286 1810
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High qality sequence stops: 314
Source: IMAGE Consortium, LLNL
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llarity 95.8%;
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Best Local Similarity
Matches 392; Conser
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20-JUN-1995

454 bp mRNA EST Homo sapiens cDNA clone 151568 3'

H03936 Yj44a05.s1 F H03936

DEFINITION ACCESSION

LOCUS

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double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not in and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.
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a; Theria;
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Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@waston.wustl.edu
High qality sequence stops: 354
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyT not found.
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteicht;
Sarcopterygli; Choanata; Tetrapoda; Amniota; Nammalia; Theria
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 454)
Hillier,L., Clark, N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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l Similarity 97.1%;
405; Conservative
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/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Ist strand cDNA was primed with a Not I: oligo(AT) primer [5' double-stranded cDNA was size selected, ligated to Eco RI dapters (Pharmacia), digested with Not I and cloned into (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Same fetus as the fetal lung library, Soares fetal lung 'allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows.'Allows
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1276 Std Error: 0.00
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                                                                                                                                                   AAUU9900 429 bp mRNA EST 01-FEB-1997
2683d06.r1 Soares fetal heart NbHH19W Homo sapiens CDNA clone
365579 5', mRNA sequence.
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Hillier.L., Clark,N. Dubuque,T., Elliston,R., Hawkins,M., Holman,M., Rucaba,T., Le.M., Lennon,G., Marra,M., Waterston,R., Williamson,A., Rohlfing,T., Tan,F., Trevaskis,E., WashU-Merck EST Project
Unpublished (1995)
                            805 gagatagtttccagaggggggaactctcatggaggtaaaaaagggaatgaagagaaaatg 864
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398 AAGAAAGACATTGGCCCGTTTGAAACTTCTCCTACCTGACCTGGCAACCCCAAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 0.00e+00;
0; Mismatches 2; Indels 1
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/clone=136559"
/scone=11b="Soares fetal heart NDHH19w"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)
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High quality sequence stop: 372.
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WashU-Merck EST Project
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Matches 399; Conservative
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SOURCE
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cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr713 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                              Osteichthyes;
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CGAA-CCTGCGAGGAGATGTGTTTTTCCCTAAGGTGAATGAAGCAGGTGAATTCGGCCTG 179
                                                                                                                                                    240 GGTTGACTGCAGCTTCAATCATNGGGATCTGTGAACTGGAAACAGGATAGACGAAGATGAT 299
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                  180 ATTCTCGGTCCAAAGGAAAGCGCTAACTTCCAAACTGGAACATAAAGATTTAAATATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotae; Metazoa; Eumetazoa; Bilateriá; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gathostomata; Osteicht!
Sarcopterygii; Choanata; Tetrapoda; Amiota; Mammalia; Theri;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 34)
Hillier,L., Clark,N., Dubuque,T., Eliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                 360 CCTTTGGCAGGTCCACAAGAAAGACATTTGGCCCGATTTGAAACTTCTCCTA 411
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WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Eax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 292
Source: IMAGE Consortium, LLNL
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Y106a03.rl Homo sapiens cDNA clone 138412 5.
9841808
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The Wash U-Merck EST Project
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60 c 8
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l Similarity 97.9%;
334; Conservative
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Bucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;

Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 442)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Hollman, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human clone=21599 library=Soares infant brain 1NIB vector=Lafmid BA
                                                                                         This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                  1249 taccggctggccggagacaaagtcgggaaacttcgagtgtttgtgaaaaacagtaacaat 1308
                                                                                                                                                                    1429 aaaaccggcgaaatcgcagtggatggcgtcttgcttgtttcaggcttatgtccagatagc 1488
                                                                                                                                                                                                                                                                                                                    181 AAAACCGGCGAAATCGCAGTGGATGGCGTCTTGTTTCAGGCTTATGTCCAGATAGC 240
                                                                                                                                                 TTGTATCAAGGAACTGATGCTACCAAAAGCATCATTTTTGAAGCAGAACGTGGCAAGGGC 180
                                                                                                                                                                                                                                                                                                241 CTTTTATCTGTGGATGACTGAATGTTACTATCTTTATATTTGACTTTGTATGTCAGTTCC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAR-1995
                                                                        GCCCTGGCATGGGAGAAGACCACGAGTGAGGATGAAAAGTGGAAGACAGGGAAAATTCAG
 TACCGGCTGGCCGANGACAAAGTCGGGAAACTTCGAGTGTTTGTGAAAAACAGTAACAAT
                   Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      yc76b01.rl Homo sapiens cDNA clone 21599 g644653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
High qality sequence stops: 305
Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 311;
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Query Match

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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1st strand cDNA was primed
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                                                                                                                                                 718 aaaaagaaggcaaaaattaaaaatgttaccccagaacccaccaggactcctaccctaag 777
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                                                                                                                                                                                                                                                                                                                                                                                                                                            838 ggtaaaaaagggaatgaagagaaaatgaaaggggggcttgaggatgagaaaagagaagag 897
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(db_xref="taxon:9606"
                                                                                    AAAAAGAAGGCAAAAATTAAAAATGTTACCCCAGAACCCACCAGGGNTCCTACCCCTAAG
                                                                                                                                                                                                                                                                                                                 186 GTGAACTTGCAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAACTCTCATGGA
                                                                                                                                                                                                                                                                                                                                                                                                   246 GGTAAAAAAGGGAATGAAGAGAAAATGAAAGGGGGCTTGAGGATGAGAAAAGAGAAAGA
                                                              /clone="IMAGE:1674607"
/clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
                       Indels
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                                                                                                                                                                                                                                                      No. 0.00e+00;
Mismatches 11;
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  Pred.
Similarity 95.8%; 345; Conservative
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                                                                                                                                        162 CAGGGAACTGACATACAAAGTCAAATATAAAGATAGTAACATTCAGTCATCCACAGATAA 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watcson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 884 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 302.
High quality sequence stop: 302.
                                                                                                                                                                                                                                                                                                                                                                                                         #0UY21 344 bp mRNA EST 17-OCT-1996
2d90b04.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone
356719 5', mRNA sequence.
W80921
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Eukaryotae; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 344),
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                           222 AAGGCTATCTGGACATAAGCCTGAAACAAGCAAGACGCCATCCACTGCGATTTCGCCGGT
                                                                                                                                                                                                                                                                                                  342 CAACTGAATTITCCCTGTCTTCCACTTTTCATCCTCACTCGTGGTCTTCTCCCATGCCAG
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                                            Length 406;
                                                                     Indels
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WashU-Merck EST Project
WashU-Merck IST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1810
Fax: 314 286 1810
                               Score 296; DB 18; Lr
Pred. No. 0.00e+00;
... matches 6;
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                                Query Match 18.4%;
Best Local Similarity 98.0%;
Matches 299; Conservative
86
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Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata: Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 347)

1 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Havelas, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."
                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                       TGCTCTTTGATTACCGGCTGGCCAC-GACAAAGTCGGCGAAACTTCGAGTGTTTGTGAAA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 AACAGTAACAATGCCCTGG-ATGGGAGAAGACCACGAGTGAGGATGAAAAGTGGAAGACA 178
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                                                                                                                                                                                                                                                                                                                                     1 AAGACATTGGCCGATTGAAACTTCTCCTACCTGACCTGCAACCCCAAAGCAACTTCTGTT
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                                                                                                                                                                                                                                                                                                                  ۷;
                                                                                                                                                                                                                                                                                Length 344;
                                                                                                                                                                    /dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares fetal heart NbHH19W"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTATGTCCAGATAGCCTTTTATCTGTGGATGACCTGAATGTNACTA 344
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                                                                                                                                                                                                                                                                        Score 285; DB 21; L
Pred. No. 0.00e+00;
0; Mismatches 8;
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                                                                                                   /db_xref="taxon:9606"
/clone="356719"
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1 Similarity 95.7%;
331; Conservative
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1 73 c
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Unpublished (1995)
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SOURCE
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                                                                                                                                                                                                                                                                                                  1224 aagcaacttctgtttgctctttgattaccggctggccggagacaaagtcggg-aaacttc 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stops: 281
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                        GGCAGGTCACAAGAAAGACATTGGCCGATTGAAACTTCTCCTACCTGACCTGCAACCCCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AAGCAACTICTGTTTGCICTTTGATTACCGGCTGGCNCAGGACAAAGTCGGGGAAACTTC 240
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1 (bases 1 to 374)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hellman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                      MO 63108
                                                                                                                                                                                              3 others
                                                                                                                                                                                                                      Score 277; DB 5; Length 34.
Pred. No. 0.00e+00;
Contact: Wilson RK
WashU-Merck Egr Project
WashUrbarty School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 bp mRNA EST
Homo sapiens cDNA clone 134534 5'
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/organism="Homo sapiens"
                                                                                                                                           Location/Qualifiers
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ilarity 95.9%;
Conservative
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R27678
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AUTHORS
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Gnathostomata; Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä;
Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 242
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1296 aaacagtaacaatgccctggcatgggagaagaccacgagtgaggatgaaaagtggaagac 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1356 agggaaaattcagttgtatcaaggaactgatgctaccaaaagcatcatttttgaagcaga 1415
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1 (bases 1 to 364)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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YA46602.r1 Homo sapiens cDNA clone 132794 5'
827153
9783288
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Pred. No. 0.00e+00;
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63 c 9
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Similarity 95.9%;
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Contact: Wilson RK
WashU-Merck EST Project
WashU-Merck EST Project
WashUngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 283
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (incompanie) for further information.
                                                                                                                                                                                                                                                                1495 tctgtgg-annnctgaatggtactatctttatattttgactttgtatgtcagttccctggt 1553
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Pred. No. 0.00e+00;
0; Mismatches 5; Indels
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1.364
//Organism="Homo sapiens"
/Clone="132794"
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est Local Similarity 96.5%;
Atches 281; Conservative
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Search completed: Sat Apr 24 23:15:07 1999 Job time : 2372 secs.